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fPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
no ou.	Sat Oct 23 14:32:42 1999; MasPar time 3416.68 Seconds
abular output ne	not generated.
litle: Description:	>US-08-702-718-1 [0.1891] from USOR702718.seq
I.A. Sequence: Comp:	1891 1 TTTTCGTTCCATCAGCCTATTATTTGATGATATTATGAA 1891 AAAAAGCAAGGTAGTCGGATAATAAACTACTATAATACTT
coring table:	TABLE default Gap 6
Match STD:	Dbase 0; Query 0
earched:	646147 seqs, 1385953633 bases x 2
ost-processing:	Minimum Match 0% Listing first 45 summaries
oatabase:	emb158 1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2 7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
oatabase:	l3:em_pl 14:em_ro 15:em_sts 16:em_vi genbanklll 17:90_bal 18:90_ba2 19:90_htgl 20:90_htg2 21:90_inl 22:90_inz 23:90_om 24:90_ov 25:90_pat 25:90_ph 27:90_pll 28:90_pl2 29:90_prl 30:90_prz 31:90_prz 32:90_ro 33:90_st 34:90_sts 35:90_sy 36:90_un 37:90_vi
Statistics:	Mean 11.454; Variance 5.068; scale 2.252

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	2.77e-187	3.19e-188	1.82e-143	
	Description	Sequence 1 from Patent	S.tuberosum mRNA for m	Sequence 3 from Patent	N. tabacum mRNA for cit	Daucus carota mRNA for	Citrus maxima citrate	Sequence 2 from Patent	B.vulgaris mRNA for ci	Arabidopsis thaliana m	Populus hybrid mRNA fo	Homo sapiens citrate s	Porcine citrate syntha	S.cerevisiae mitochond	
SUMMARIES	ΩI	A46545	STCITS	A46547	NTCITSYNH	AB017159	CMU19481	A46546	BVCITSYNH	ATMTCITRN	PHCITSYNH	AF047042	PIGCITSYN	SCMTCISNA	
	DB	25	27	25	27	27	27	25	27	27	27	31	23	27	
	Query Match Length DB	1891	1891	1747	1747	1859	1733	1551	1551	1680	1378	1401	1455	1481	
æ	Query	100.0	100.0	65.5	65.5	39.6	37.0	35.1	35.1	29.9	29.8	12.7	12.7	10.2	
	Score	1881	1891	1238	1238	748	700	664	664	266	564	240	241	193	
	Result No.	-	7	æ	4	S	9	7	80	6	10	11	12	13	

Yeast gene for citrate 1.82e-143 2 S.cerevisiae chromosom 1.82e-143 2 S.cerevisiae N2019, N2 1.82e-143 2 S.pombe chromosom 1.82e-143 2 S.pombe chromosom 2.190e-131 Candida tropicalis DNA 5.33e-125 S.cerevisiae) C 4.69e-93 S.cerevisiae) C 4.69e-93 Yeast (S.cerevisiae) C 4.69e-93 Yeast (S.cerevisiae) C 4.69e-93 Norassa mitochondrial 3.38e-59 N Crassa mitochondrial 3.38e-59 N Luyveromyces lactis D 7.74e-55 Caenorhabditis elegans 2.34e-45 21 Arabidopsis thaliana c 4.18e-41 Caenorhabditis elegans 4.64e-35 N S.cerevisiae citrate S 3.36e-26 S.cerevisiae citrate S 3.36e-26 S.cerevisiae citrate S 3.36e-26 S.cerevisiae chromosom 3.36c-26 S.cerevisiae chromosom 4.38e-19 Sequence 14 from paten 9.66e-14 Sequence 22 from paten 6.35e-10 Drosophila melanogaste 2.94e-05 Drosophila melanogaste 2.94e-05 Drosophila melanogaste 2.39e-04 Arabidopsis thaliana '2.53e-03	TS  4487.  PAT 07-MAR-1997  Teptophyta; Embryophyta, Trachecphyta a, Magnoilophyta, eudicctyledons, les; Solanaceae; Solanum; Potatoe; tze,V. and La,C.U. FOR INDUCING FLOWER FORMATION IN P-1995; (DE) 950925 950928 950914.  tuberosum" EE" 3" NYHHASE" YNTHASE"
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LLFLGNLAKLKPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG
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                                                                                                                                                       LVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGG
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1861 TTTGCTAATTCTTATTTGATGATATTATGAA 1891

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LVAAYVYRRWYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGG
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
section Petota
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Submitted (20-SEP-1993) V. Landschuetze, Inst. fuer Genbiologische
Forschung, Berlin GmbH, Ihnestr. 63, 14195 Berlin, FRG
2 (bases 1 to 1891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Landschutze,V., Muller-Rober,B. and Willmitzer,L.
Mitochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds
Planta 196 (4), 756-764 (1995)
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                                         S.tuberosum mRNA for mitochondrial citrate-synthase. X75082
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Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 1747)
Mueller-Roeber, B. Landschuetze, V and La.C U
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
                                                                             1381 CTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGCTCTTGGATTGCCGCTAGAGAGGCCA 1440
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                                    1321 AACTATTATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGCGTATCAAGAGCT
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SAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEBCGENISKEOL
KDYAMKTLKSGKVVPGFGHGVLKKTDPRYTCQREFALKHLPEDPLFGLVAKLYEVTLU
FLQNLAKTNRWPNVDHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGL
LERPKSVTMEWLENHCKKA"
                                                                                                                         QELIPEQQDELKKLKSEHGKVQLSNITVDMVLSGMPGMTGLLWETSLLDPDESIPFPS
LSIYECQKVLPAAKPGGEPLPEGLLMLLLTGKVPSKEQVDSLSQELRSRATVPDHVYK
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euphyllophytes: Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 1747)
La Cognata U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                1107 GGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGCAAGACTGATCCAAGATACACATGCCA 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1116 GGTTGTCCCTGGTTTTGGACATGGAGTTCTGCGAAAGACTGTACCAAGATATACATGCCA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1287 IGAIGCCCACAGIGGIGIGIIGIIGAACIAITAIGGIITTAACIGAAGCAAGAIAIIAIAC 1346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1416 TCTTGGATTGCCGCTAGAGGGCCAAAGAGTGTCACAATGGAGTGGCTTGAGAACCAGTG 1475
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876 AATACACAGTGATCATGAAGGTGGTAATGTCAGTGCTCACACGGGTCACTTGGTTGCTAG 935
                                                                                                                                                   927 IGCITIGICAGACCCTIACCICICCTICCCTGCCTGCTTIGAAIGGITIAGCIGGACCACT 986
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Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
                                                                                                                                                                                                936 IGCTITGICISAICCITACCICTCCCTITGCIGCIGCITIGAAIGGITIAGCCGGACCACI
                                                                                                                                                                                                                                         TCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGASGAGTGTGG
                                                                                                                                                                                                                                                                                    996 TCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCTGTTGTAGAAGATGTGG
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                                                                 867 GATACACAGTGATCATGAAGGTGGTAACGTCAGTGCTCACACAGGTCACTTGGTTGCTAG
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La Cognata, U.
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Berlin, FRG

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FLQNLAKLNPWFNVDAHSGVLLNYYGLTEAPYYTVLFGVSPALGIGSQLIWFFALGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 CTGTCAAAGCTGCGTTGTCGAGCGGTCCAACACACAAATCTTAGCAACTCTGTGCGGTGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 CTGTCAAAGCTCCGCTCTCGAGCGGTCCAACAGTCAAATGTTAGCAATTCTGTGCGCTGG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 CTICAAGTCCAAACCICTICIGGICTIGAICIGGGITCIGAGCIG---CAAGAATIGAIT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 CTTCAAGTCCAAACCTCTTCCGGTCTTGATCTGCGTTCTGAGCTGGTACAAGAATTGATT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 CCAGAACAACAGGATCGCCTAAAGAAGCTCAAGTCAGAGCATGGAAAGGTTCAATTGGGA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 AACATCACAGTTGATATGGTTCTTGGTGGAATGAGAATGACAGGATTACTGTGGGAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 A-CATCACAGTTGATATGGTTCTTGGTGGAATGAGAGGAATGACAGGATTACTGTGG-AA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 CCAAAAGGIATTACCIGCAGCAAAGCCIGGGGGAGAGCCCTIGCCIGAAGGICTICICIG 452
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                                                  /organism-"Nicotiana tabacum"
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                                                                                                                                                                                                                                                                    /product="citrate synthase"
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/db_xref="G1:1556429"
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Location/Qualifiers
1. .1747
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                                                                                 /cultivar-"SNN"
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70. .1479
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Matches 1439; Conservative
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1347 GGTCCTCTTTGGTGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGC 1406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      987 TCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTGG 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1047 GGAGAACATTTCCAAAGAGCAGTTGAAAGACTACGCTTGGAAAACATTGAAAAGTGGCAA 1106
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                                                                          690 GGATTCCATGAGTTTGATTGCTCAAGTTCCACTTGTTGCTGCTTATGTTTATCGCAGGAT 749
                                                                                                                              696 GGATTCCATGAATCTGATTGCTCAAGTTCCACTTGTTGCTGCTTATGTTTATCGCAGGAT 755
                                                                                                                                                                               750 GTACAAGAAGGCAACACTATACCTAAGGATGACTCACTGGATTATGGTGCAAATTTTGC 809
                                                                                                                                                                                                                                                                                     810 TCACATGCTTGGTTTCAGTAGCTCTGACATGCATGAGCTT---ATGAAGCTCTATGTCAC 865
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                     636 ATTICAAAAGGCATACGAGAAAGGGATTCACAAATCAAAGTATTGGGAACCAACATATGA 595
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Daucus carota mRNA for citrate synthase, complete cds.
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Daurus carota (cultivar.MS Yonsun) suspension cultured cells cDNA
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/db_xref="GI:3493367"
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VVAAYIYRRMYKNGQSISTDDSLDYGANFAHMLGYDSPSMQELMRLYVTIHTDHEGGN
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                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Araliales; Aplaceae; Daurus I (bases 1 to 1859)
Takte, E., Koyana, H., Shirano, Y., Shibata, D. and Hara, T. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps 10;
                                                                                                                                                                             Submitted (26-AUG-1998) to the DDBJ/EMBL/GenBank databases. Eiji Takita, Gifu University, Laboratory of Plant Cell Technology, Faculty of Agriculture: Yanaqido 1-1, Gifu, Gifu, 501-1193, Japan (E-mailtakitadec.qifu-u.ac.jp, Tel:+81-58-293-2911, 22 (bases 1 to 1859)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 GAGAAATGGTGTTTTTGGAGTGTTTGGGTGGTTAAGAAGGTGGGGTGTGGGGGTGTTG
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/db_xref="taxon:4039"
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452 TTCGCTTTAGGGGGTTGTCCATACCTGAATGTCAGAAGCTATTACCAGGAGCGAAGCCCG 511
                                               365 TTCGCTTCCGGGGGTTGTCTATACCTGAATGCCAAAAGGTATTACCTGCAGCAAAGCCTG 424
                                                                                                                     425 GGGTGAGCCCTTGCCTGAAGGTCTTCTCTGGCTTCTTTAACAGAAAGGTGCCATCAA 484
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Canel,C., Bailey-Serres,J. and Roose,M. Physiological and molecular genetic studies of acid accumulation in
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SAHYGHLVABALSDPYLSFFAALNGLAGPLHGLANDEVLLHWRSYVDEGCENVYTEQL
SDHYGHLANSGKVVPGEGHGYLRKTDPRYTCQREFALKHLPDDPLFGLVSKIYEVVPP
ILTKLGKVKNPWPNVDAHSGVLLNHFGLAEARYYTVLFGVSRSLGICSQLIWDRALGL
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KEMIPEQOERLKKVKSDLGKAQLGNITIDVVIGGMPGMTGLIWETSLLDPDFGIPFPG
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AIDALPVSAHPWTQFASGVMALQVQSEFQEAYEKGIHKSKSWEPTSEDSLNLJARVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               citrus fruits
Thesis (1994) Botany & Plant Sciences, University of California at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-JAN-1995) Camilo Canel, University of California at Riverside, Botany & Plant Sciences, Riverside, CA 92521-0124, USA Location/Qualifiers
                                                                             CMU19481 1733 bp mRNA PLN 04-DEC-1995
Citrus maxima citrate synthase (cit) mRNA, nuclear gene encoding
mitochondrial protein, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="There is a single copy of the cit gene in the citrus genome. A single transcript with an estimated length of 1,850 nucleotides can be detected in juice cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="synthesis of citrate from oxaloacetate and
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                         1442 AGAGTGTCACAATGGAGTGGCTTGAGAACCAGTGCAAGAAAGCATGAATTGTTTGAAA 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function="targets the protein to the mitochondrial
                                                                                                                                                                                                                                                                                                                     Citrus maxima Eukaryotes; Viridiplantae; Charopita/etaryotae; Mitochondrial eukaryotes; Viridiplantae; Charopita/Embryophyta; Magnoliophyta; Magnoliopsida; Rutanae; Sapindales; Rutaceae; Citrus. 1 (bases 1 to 1733)
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/protein_id="AAA82743.1"
/db_xref="PID:9624676"
/sex-"hermaphrodite"
/cell_type-"juice cell"
/tissue_type-"juice tissue"
/dev_stage="immature"
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                                                                                                                                                                                                                                      68 GAGCAATGGTGTTCTACCGTAGCGTTTCGTTGCTGTCAAAGCTCCGGTCTCGAGCGGTCC 127
                                                                                                                                                                                                                                                                                                                                  128 AACAGTCAAATGTTAGCAATTCTGTGCGCTTGGAGGTCCAAACCTCTTCCGGTCTTG 187
                                                                                                                                                                                                                                                                                                                                                                                  172 ACCTTCATTCTCAGCTC--A-AGGAAATGATTCCAGAACAACAGGGGCGCTGAAGAAAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                  188 ATCTGCGTTCTGAGCTGGTACAAGAATTGATTCCTGAACAACAGGATCGCCTGAAAAAGA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 GGATGAGAGGAATGACTGGCTTACTTTGGGAAACCTCATTAC-TTGACCCTGATGAGGGA 347
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/db_xref="PID:92300710"
/db_xref="G1:2300710"
/translation="SSNLDLRSELGELIPEQOEPLKKIKKEFGSF@LGNINVHWVLGG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                                                       1381 CTIGGCATITGCICICAGCIAATITGGGACCGAGCICTIGGATIGCCGCIAGAGAGGCCA 1440
                      1024 CTATGGATAAAATCTGTTGTAGAAGAATGTGGGGAGAACATTTCCAAAGAGCAGTTGAAA 1083
                                                                             1062 GATTATGTCTGGAAAACATTGAATAGTGGCAAGGTTGTCCCTGGATTTGGTCATGGTGTT 1121
                                                                                                                           1084 GACTATGTTTGGAAAACATTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGGAGTT 1143
                                                                                                                                                                                1122 TTGCGTAAAACTGATCCGAGATACACTTGTCAGAGGGAGTTTGCCTTGAAGCATTTGCCT 1181
                                                                                                                                                                                                                 1182 GATGATCCATGTTCTAGGTTTCTAAGCTGTATGAAGTGGTGCCCCCAATATTAACA 1241
                                                                                                                                                                                                                                                                                                                                       1204 GAAGATCCACTGTTTCAACTGGTTTCAAAACTCTACGAAGTTTTCCTCCTCTTTA-CA 1262
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Mueller-Roeber, B., Landschuetze, V. and La, C.U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
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1422 AAAAGTGTAACTTTAGATTGGATTGAGAAAATTGCAAGAAAGCA 1466
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/strain="zUCHTLINIE 5S 0026"
/db_xref="taxon:3555"
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/db_xref="PID:e306423"
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HOECHST SCHERING AGREVO GMBH (DE)
Other publication DE 4438821 960425
Other publication DE 4435366 960328
Other publication AU 2067995 950925
Other publication DE 4408629 950914.
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Sequence 2 from Patent W09524487.
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/clone="PSBCS"
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DSPOMLELMELYTHSDHEGGNVSHTGHLVGSPLSDPTLSFAALNGLAGFLHGLA
NOGVLLHTKSVVDECGENTSTEGLKBVVWRTLNSGKVVPGFELGVLPRTDPPTTCRF
FALKHLPDDPFPFQLYSKLYFWPPTLLELGKVKNPRPWDAHGGVLLNHYGLTZARYY
TVLFGVSRSLGICSQLIWDRALGLPLERPKSVTMEWLEKFCKRRA"
SKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEK
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Pred. No. 0.00e+00:
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/db_xref="SPTREMBL:096544"

ft.anslation="SSNLDLRSELQELIPEODERLKKIKKEFGSFOLGNINVDMVLGG
MRGMTGLLWETSLLDPEBGIRFRGFSIPPECOKLLPAASAGABFLPEGLLWLLLTGKVP
SKEQVDALSADLRKRASIPDHVYKTIDALPITAHPWTGFCTGWAALQTRSEFOKAYEK
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DSPOMLELMRLYVIIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLA
NQEVLLWIKSVVDECGENISTEQLKDYWKTLNSGKVVPGFGLGVLRKTDPRYTCQRE
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1 (bases 1 to 1551)
1 (bases 1 to 1551)
1 a Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B. Plant Cell Physiol. In press
2 (bases 1 to 1551)
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                                              1103 TGAACAGTGGCAAGGTTGTCCCTGGTTTTTGGACATGGAGTTCTGCGAAAGACTGTACCAA 1162
                                                                                               983 GATACACATGCCAAAGAGAATTTGCGTTGAAGCACTTGCCTGATGACCCATTTTTTCAAT 1042
923 TAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAA 982
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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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/protein_id="CAA59010.1"
/db_xref="PID:e137433"
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/db_xref-"GI:1556380"
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1103 TGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGGAGTTCTGCGAAAGACTGTACCAA 1162
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TVLFGVSRSLGIGSQLIWDRALGLPLEPPKSVTMEWLEKFCKRRA"
258 c 370 g 458 t
                                                                                                                                                                0; Mismatches 261; Indels 12;
                                                                                                             Length 1551;
                                                                                                          Score 664; DB 27;
Pred. No. 0.00e+00;
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Similarity 78.5%;
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NVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKE
QLKEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQPRFALKHHPDDPLFGGCKLMKLAS
CLTELESEEPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA
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PVVAAYVYRRMYKNGDSIPSDKSLDYGANFSHMLGFDDERLKELMRLTSPSTVMHEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana
                                                                                                                                                                                                                             TTATATGGGACCGAGCTCTTGCCTTGCCGCTAGAGGCGCCAAAGAGTGTCACTATGGAAT 1282
                                                                                 1043 TGGTGTCAAAGTTGTATGAAGTGGTGCCTCCTATTCTATTAGAGCTTGGAAAGGTAAAGA 1102
                                                                                                                                   1223 IGGTITCAAAACICIACGAAGITIT-CCTCCTGTICTTACAGAACTTGGCAAAGITAA-A 1280
                                                                                                                                                                                             1103 ATCCATGGCCTAATGTTGATGCTCATAGTGGAGTTTTGCTGAACCACTATGGTTTGACAG 1162
                                                                                                                                                                                                                                                                                                      1163 AAGCAAGATACTATACGGTTTTGTTTGGGGTATCAAGGAGTCTTGGAATATGCTCACAGC 1222
                                                                                                                                                                                                                                                                                                                                                          1340 AAGCAAGATATTATACGGTCCTCTTTGGCGTATCAAGAGCTCTTGGCATTTGCTCTCAGC 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1400 TAATTTGGGACCGAGCTCTTGGATTGCCGCTAGAGGCCCAAAGAGTGTCACAATGGAGT 1459
                          1163 GATATACATSCCAGAGAGAGTTCGCTATGAAGCATTTGCCTGAAGATCCACTGTTTCAAC 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS ATMICITRN 1680 bp mRNA PLN 26-NOV-1997
DEFINITION Arabidopsis thaliana mRNA for mitochondrial citrate synthetase.
ACCESSION X17528
Unger, E. A., Hand, J.M., Cashmore, A. R. and Vasconcelos, A. C.
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/db_xref="taxon:3702"
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/product-"citrate synthetase"
/protein_id="cap35570 1"
/db_xref="PID:e1188578"
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Best Local Similarity 75.6%;
Matches 1087; Conservative
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X17528.1 GI:11243
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57 AATGGTGTTTTTCCGCAGCGTATCGGCCTTTACTAGGCTGAGGTCTCGCGTCCAGGGCCA 116

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943 ICATITGCAGCIGCATTAAAIGGITTAGCIGGGCCACTCCAIGGITIGGCIAATCAGGAA 1002
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                                                 117 ACAATCTTCACTCAGCAATTCTGTCAGATGGATTCAGATGCAGAGCTCTACCGACCTGGA 176
                                                                                 189 TCTGCGTTCTGAGCTGGTACAAGAATTGATTCCTGAACAACAGGATCGCCTGAAAAAGAT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 CCIGGGGGGGAGG-CCIIGCCIGAAGGTCIICICIGGCTICIIITAACAGGAAAG4TGCC 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779 CTAAGGATGAATCCCTGGATTATGGTGCAAATTTTGCTCACATGCTTGGTTTCAGTAGCT 838
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72 AATGGTGTTCTACCGTAGCGTTTCGTTGCTGTCAAAGCTCCGGTCTCGAG--C-GGTCCA 128
                                                                                                                                                177 CCTGAAGTCGCAGCTG---CAAGAGTTAATTCCGGAACACAAGGACCGTCTGAAGAAACT 233
                                                                                                                                                                                                                                                 234 GAAGTCAGAACATGGGAAGGTCCAACTGGGAAACATCACTGTTGATATGGTTATTGGTGG 293
                                                                                                                                                                                                                                                                                              249 CAAGICAGAI-AIGA-AAGGIICAAIIGGGAA-CAICACAGIIGAIAIGGIICIIGGIGG 305
                                                                                                                                                                                                                                                                                                                                                   294 AATGAGAGGATGACTGGATTGCTTTGGGAAACCTCATTGC-TTGACCCGGAAGAGGTA- 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 TICGCITIAGGGGAITGICGACITCCIGAGIGCCAGAAAGCCCIAITACCIACIGCCCAG 411
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/translation="MPTKEQVGALSKELRDRALVHDYVFKAIDALPVTAHPMTQFATG
VMALQVQSEFQKAYEKGIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPM
NDSLVIGGNFSHMLGFDSPEMQELMRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLS
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HGVLRKTVPRYTCQREFALKHLPDDPLFQLVSKLYEVVPPVLTQLGKVKNPWPNVDAH
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populus balsamifera subsp. trichocarpa X Populus deltoides.

Populus balsamifera subsp. trichocarpa X Populus deltoides.

Populus balsamifera subsp. trichocarpa X Populus deltoides

Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Rosidae, Violales; Salicaceae; Populus.

1 (bases I to 1378)

La Cognata I, Landschuetze, V, Willmitzer, L and Wieller-Roeber, B.

2 (bases I to 1378)
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                                             1198 ITGCCTGAAGATCCACTGTTTCAACTGGTTTCAAAACTCTAGGAAGTTTTCCTCTGTTC 1257
                                                                                                      1238 TCACTGAGCTTGAAAGTGA-AGAACCCTGGCCAAATGTTGATGCTCACAGTGGGGTCTTG 1296
                                                                                                                                                         1258 TTACAGAACTIGGCAAAGTTAAAACCTIGGCCAAAIGTIGAIGCCCACAGIGGIGIGITG 1317
                                                                                                                                                                                                             1297 CIGAACCACTAIGGICIAACCGAAGCAAGGIACTACACCGIGCICTIIGGIGIIICAAGG 1356
                                                                                                                                                                                                                                                                   1318 TIGAACTATTATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGCGTATCAAGA 1377
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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63,
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/protein_id-"CAA59009.1"
/db_xref-"PID:e276838"
/db_xref-"PID:g1649926"
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Populus hybrid mRNA for citrate synthase.
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DB 27; Length 1378

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608 AACAACTTAAAGACTATGTTTGGAAAACATTAAATAGCGGAAAGGTTGTTCCTGGATTTG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            668 GTCATGGAGTTCTACGCAAAACTGTACCAAGATATACATGTCAAAGGGAGTTTGCATTGA 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908 TATCAAGGAGTATTGGCATFTGCTCTCAGCTGATATGGGATCGAGCTCTTGGATTGCCGC 967
                                                                                                                                                                     72 GGTTCATGATTATG-TCTTTAAGGCCATTGATGCCTTACCTGTCACTGCTCATGA 130
                                                                                                                                                                                                                                                                                                                                                                                                               653 AGAAAGGGATTCACAAATCAAAGTATTGGGAACCAACATATGAGGATTCCATGAATCTGA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          713 TIGCICAAGIICCACIIGIIGCIGCIIAIGIIIAICGCAGGAIGIAACAAAIGGIGACA 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           773 CIATACCTAAGGAIGAAICCCIGGAITAIGGIGCAAAITIIGCICACAIGCIIGGIIICA 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 ATAGTCCTGAAATGCAAGAGCTT -- - ATGAGGCTTTATGTTACTAACCATAGTGACCATG 427
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                                                                                                                    473 AGGTGCCATCAAAAGAGCAAGTGAATTCAATTGTCTCAGGAATTGCAGAGTGGGGCATCA 532
                                                                                                                                                                                                                  533 TATCCCTGATCATCATGTATACAACTATTGATGCCTTACCAGTCACAGCTCATCCAATGA 592
                                                                       14 AGGIACCAAACAAAAAAGCAAGTGGGTGCC-TTATGGAAGGAATTGCGTGACCGTGC-TCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 ATCTTTCATTTGCAGCTGCATTGAATGGTTTAGCTGGGCCACTCCATGGCTTGGCAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        788 CAGTICITACCCAGCIGGGCAAGGIIAAAAACCCAIGGCCIAAIGIIGAIGCICACAGIG
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Best Local Similarity 80.0%; Pred. No. 0.00e+00;
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RESULT

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/translation-"MALLTAAARLLGTKNASCLVLAARHASASSTNLKDILADLIPKE
QARIKTFRQQHGKTVVGQITVDMMYGGMPGMKGLVYETSVLDPNEGIPFPGFSIPEYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLHPMSQLSAAVTALNSESNFAQAYARGISRTKYWELIYEDSVDLIAKLPCVAAKIYR
NLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVGSALSDPYLSFAAAMNGLAGPLHGLANOEVLWLTOLOKEVGKDVSDEKLRDY IWN TALNGGRVPGOTGHAVLERTDFRYTCOREFALKHLPNDPMFKLVAGLYKTVPNLLEDG KAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAOLIWSRALGFPLERPK SMSTEGLMKFVDSKSG"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-FEB-1998) Molecular Cardiology Institute, 75 Raritan Avenue, Highland Park, NJ 08904, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 AGCTCATCCAATGACCCAGTTTGCTACTGGAGTCATGGGTGTTGAGGTTGAAGTGAATT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 AICACTGTGGACATGTATGTTGTGCGCATGAGGCATGAAGGATTGGTGTATGAAACA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 AICACAGTIGATATGGTTCTTGGTGGAATGAGAGGAATGACAGGATTACTGTG-GAAACC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 GCTGGTAACTGGATGTATCCCAACAGGAACAGGTATCTTGGCTC-TCAAAAGAGTGGG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 TCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAATTGTCTCAGGAATTGC 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 CAAAGAGGCAGC-TCTGCCTTCCCATGTGGTC-ACCATGCTGGACAACTTTCCCACCAA 482
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                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1401)
  05-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ICAGTIC-TIGAICCIGATGAGGGGATCCGTTTTCGGAGGCTTTAGTATCCTGAATGCCA
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                                                                                                                                                                                                                                                                                               Cloning and sequence analysis of human citrate synthase Unpublished
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                         Homo sapiens citrate synthase mRNA, complete cds.
AF047042
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/note="isolated from a 22-year old"
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/protein_id-"AAC25560.1"
/db_xref-"PID:g3288815"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"taxon:9606'
/sex-"male"
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1401 bp
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Direct Submission
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artlodactyla; Suiformes; Suina; Suidae; Sus. 1 (bases 1 to 1455)
Evans, C.T., Owens, D.D., Sumegi, B., Kispal, G. and Srere, P.A. Isolation, nucleotide sequence, and expression of a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1019 GGGTTGTTCCAGGCTATGGCCATGCAGTACTAAGGAAGACTGATCCGCGATATACCTGTC 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1139 IGTACAAGATIGIGCCCAAIGICCTCTIAGAGCAGGGTAAAGCCAAGAAICCTIGGCCCA 1198
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                                                                                                                                                                                                                                 759 CAAGAATGGTGACACTATACCTAAGGATGAATC---CCTGGATTATGGTGCAAATTTTGC 815
                                                                                                                                                                                                                                                                                     723 CAACATGTTAGGCTATACT-GATCATCAGTTCACTGAGCTC--ATGCGCCTGTACCTCAC 779
                                                                                                                                                                                                                                                                                                                                                                                           780 CATCCACAGTGACCATGAGGGTGGCAATGTAAGTGCCCATACCAGCCACTTGGTGGGGCAG 839
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                                                                             603 ITCTGTGGATCTAATAGCAAAGCTACCTTGTGTTGCAGCAAAGATCTACCGAAATCTCTA 662
                                                                                                                              699 TICCATGAATCTGATTGCTCAAGTTCCACTTGTTGCTGCTTATGTTTATCGCAGGATGTA 758
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876 AAIACACAGIGATCATGAAGGIGGIAAIGTCAGIGCTCACACCGGICACTIGGIIGCIAG
                                                                                                                                                                             663 CIGGGAAGGCAGCGGTATTGGGGCCATTGACTCTAACCTGGACTGGTCTCACAATTTCAC
                                                                                                                                                                                                                                                                                                                                       816 TCACATGCTTGGTTTCAGTAGCTCTGAAATGCATGAACTTCTTATGAGGCTCTATGTAAC
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Porcine kidney, cDNA to mRNA, clone PCS4.
Sus scrofa
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Biochemistry 27, 4680-4686 (1988)
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KMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPT
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NLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSH
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TLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNVLLEQG
KAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPK
                                                                                                                                                                                                                                                                                          /translation-"MALLTAAARLFGAKNASCLVLAARHASASSTNLKDILADLIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 241; DB 23; Length 1455;
Pred. No. 3.19e-188;
0; Mismatches 416; Indels 14; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 CATTACCTTGACCCTGATGAGGGAATTCGCTTCCGGGGGTTGTCTATACCTGAATGCCAA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 AAAGAGGGCAGC-TCTGCCTTCCCATGTGGTC-ACCATGCTGGACAACTTTCCCACGAAT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 GAGTCGGGCATCATATCCCTGATCATCATGTATACAACTATTGATGCCTTACCAGTCACA 579
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                                                                                                                                               /note="citrate synthase precursor (EC 4.1.3.7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="citrate synthase signal peptide"
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                                                                                                                                                                                                   /proteIn_id="AAA31017.1"
/db_xref="PID:g164419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="citrate synthase"
                                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
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Location/Qualifiers
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Matches 741; Conservative
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 1481)
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                                                                                                                                                                                                                                                        1026 GGTTGTCCCAGGCTATGGCCACGCAGTACTAAGGAAGACTGATCCACGATATACCTGTCA 1085
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                                                                                                                                                                     966 CAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCTGGAATACACTCAACTCAGGACG 1025
                                                                                                                                                                                                                                                                                                                                                                                   1176 GAGAGAGTIUGUTATGAAGUATTIGUCTGAAGATCCACTGTTTUAACTGGTTTGAAAACT 1235
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                    847 GCCCTITCAGACCCCTACTIGICTITGCAGCAGCCAIGAAIGGGCTGGCAGGGCCCCTA 906
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Lindner,P and Plueckthun,A.
The effect of point mutations in the hinge of yeast citrate
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Submitted (05-JUL-1993) Peter Lindner, Protein Engineering,
Max-Planck Institut fuer, Biochemie, Am Klopferspitz 18a,
Martinsried, D-82152, Fed. Rep., Germany
4 (Pases 1 to 1481)
Suissa,M., Suda,K. and Schatz,G.
                                                                                                                                                                                                           1057 GAGA-ACATTTCCAAAGAGCAGTTGAAAGACTATGTTTGGAAAACATTGAACAGTGGCAA
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                                                                                  907 CATGGGTGGCAAATCAGGAAGTGCTTGTTTGGCTGACA-CAGCTGCAGAAGGAAGTCGG
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3 (bases 1 to 1481)
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Z23259.1 GI:313749
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/db_xref="taxon:4932"
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GGROVSAHTHLVGSALSSPYLSLAAAGLNGBAGPLHGRANQGVLEWLFKLREEVKGDY
SKGTVSAMTLAMPLLANGRVVPGFQAAVLRYDPRYTAGRFALKHFPDYELFKLYSTIY
EVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPOUTIY
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direct N-terminal protein sequencing"
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/product-"nitochondrial litrate synthase"
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/organism="Saccharomyces cerevisiae"
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Local Similarity 61.2%; Pred. No. 1.82e-143;
es 703; Conservative 0; Mismatches 432;
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                      /strain="D273-10B
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Saccharomyces cerevisiae
Eukaryota; Fungi, Ascomycota; Hemiascomycetes; Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1138 GGAGTICTGCGAAAGACTGTACCAAGATATACATGCCAGAGAGTTCGCTATGAAGCAT 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1135 TICCCAGATTACGAGTTATTTAAGTTGGTCTCCACCATTATGAAGTTGCCCCAGGGGTT 1194
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                                                  599 IIGCTACTGGAGTCATGGCTCTTCAGGTTCAAAGTGAATTTCAAAAGGCATACGAGAAAG 658
                                                                                                     599 GIGTATCCAAGAAAGAATATIGGAGCTATACATTIGAAGATICGTIAGATCTGCIGGGGTA 658
                                                                                                                                                     659 GGATTCACAAATCAAAGTATTGGGAACCAACATATGAGGATTCCATGAATCTGATTGCTC 718
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                                                                                                                                                                                                                                                        719 AAGTICCACTIGIIGCIGCIIATGIIIAICGCAGGAIGIACAAGAAIGGIIGACACIAIAC 778
                                                                                                                                                                                                                                                                                                           719 CAACCGATCCTAATGCTGACTATGGTAAAATTTGGCCCAACTTTTGGGCTACGAAAACA 778
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539 ITICIATIGCCGIGACTGCTTTAGAAAGCGAGTCTAAGTTIGCCAAAGCATAIGCTCAAG 598
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LGKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSD
HEGGNVSAHTTHLVGSALSSPYLSLAAGLNCLACPLHGRANQEVLEWLFKLREEVKGD
YSKETIEKYLWDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTI
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DRAVGAPIERPKSFSTEKYYKELVKKIESKN"
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/translation-"mSalLSTTSKSFLSRGSTRQCQNMQKaLFALLNARHYSSASEQT
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l (bases 1 to 2427)
Suissa,M., Suda,K. and Schatz,G.
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening method
EMBO 1.3 (8), 1773-1781 (1984)
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                                                                                                                                                                                                 Data kindly reviewed (09-MAY-1985) by G. Schatz
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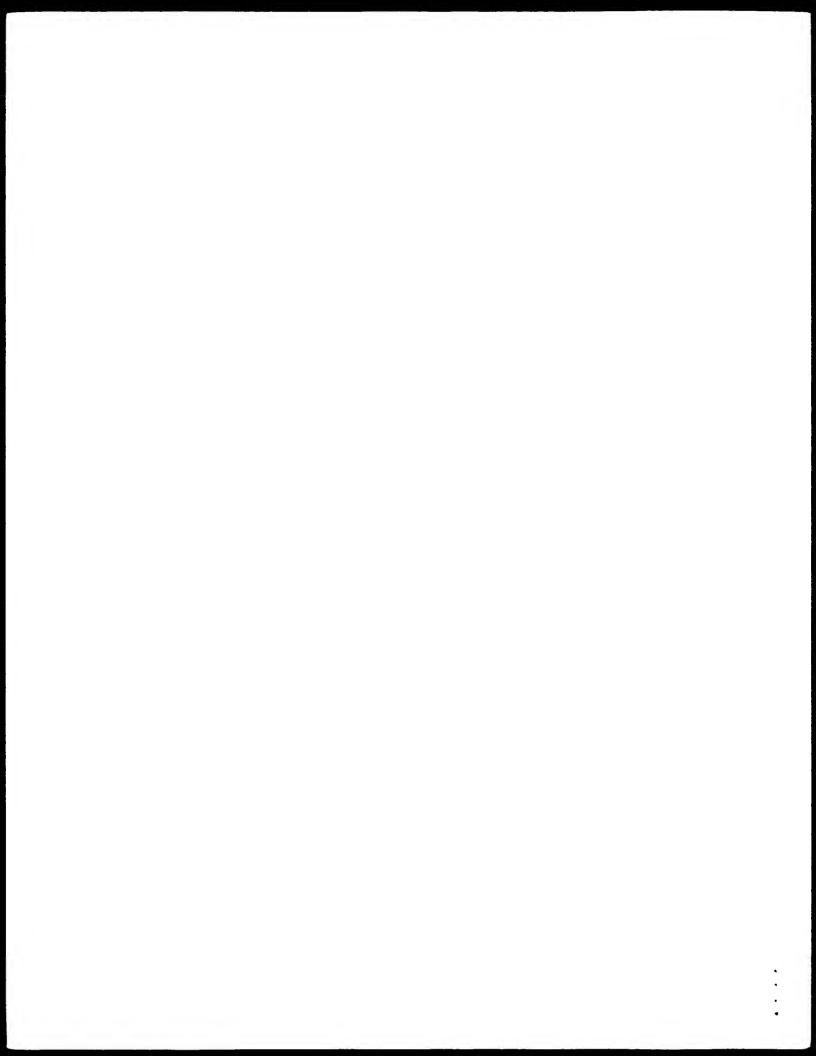
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                959 CCTTTGCTGCTGCTTTGAATGCTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAG 1018
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                                             899 GTAATGTCAGTGCTCACTGGTTGGTTGGTTGGTTGTTGTCTTGTCTTACCTCT 958
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S cerevisiae chromosome XIV reading frame ORF YNROOLC.
271666 <u>y13139</u>
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Aert, R , Verhasselt, P., Voet, M. and Volckaert, G.
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EHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKLPYTASKIYRNVFKDGKITSTDPNADYGRNLAQLLGYENKDFIDLMRLYLTIHSDH
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SKETIEKYLMDTLNAGRYVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLI11D
RAVGAPIERPKSFSTEKYKELVKKIESKN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1322 TTCAACACACACCACTGTGGGCATCAACATTTGGCCAAGG-TT-TTAACTTTGCCAAGT 1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3230. .3301)
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/note="anticodon gene: AGG; tRNA-Pro2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //octe-fanticodon gene: GTT; tRNA-Asn
3983. 4056
/gene=fucgTJNR - systematic name"
803 c 784 g 1392 t
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                                                                                                                                                                                                                                                                                                                                                               /db_xref-"GI:1302469"
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                      235. .259 // note="CEN element CDE III"
/note="CEN element CDE II"
                                                                                                                                                                                                                                                                                      /protein_id="CAA96277.1"
/db_xref="PID:e239778"
                                                                                                                                                                                                                                                                                                                                           /db_xref-"PID:g1302469"
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complement(3503. .3873)
/note="solo-tau"
                                                                  complement(1006. .2445)
                                                                                                                          /db_xref-"SGD:L0000341"
                                                                                                                                                      complement(1006. .2445)
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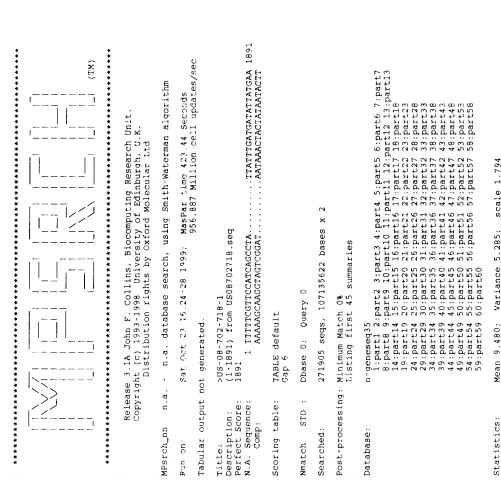
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1603 AACGTTACCACCTTCATGATCAGATGAATAGATAAAATATAGTCTCATTA--AGTCAATA 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1900 AATAGAAAATTGCGCCATTGGATGTAGATCTTTTGGGAGGCTATCTAAAAGTTGGATA-A 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2016 CGTCAGTAGGTATTTCACCAGTCAAAAGCAACCAAAATAAAGCTTCTGGCAAAGGTTCTG 2075
1483 ITCTAAAACTICTIGAITGGCACGACCAIGTAATGGGCCAGCIAAACCAITCAAACCAGC 1542
                                                                                     1543 GGCCAAAGATAAGTATGGCGAAGATAAGGCAGAACCCACTAAATGTGTAGTATGGGCAGA 1602
                                                                                                                                                                                                                                                             1661 AAAICCTIGTTTTCGTAGCCCAAAAGT-TGGGCCAAATTTTTACCATAGTCAGCATTAGG 1719
                                                                                                                                                                                                                                                                                                                                                     1720 ATCGGTTGAAGTAATTTTACCATCCTTGAACACATTACGATAAATTTTGGAAGCAATAAC 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                          1840 GGAIACACCTTGAGCATATGCTTTGGCAAACTTAGACTTGGCTTTCTAAAGCAGTCACGGC 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1959 CG-TGCTCTGGAATITCTGATCTGGCAGCTAAAT-CAGCAGA-AAGGGCTTTAACTTGAG 2015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2136 TAATACCTTCTTCGGGGTCTAACACGGAACCTTCCCAAACAAGGCCTTTAATACCTCTCA 2195
                         606 AGTAGCAAACTGGGTCATTGGATGAGCTGTGACTGGTAAGGCATC-AATAGTTGTATACA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 906 GACATTACCACCTICATGATCACTGTGTTACATAGAGCCTCATAAGAAGTTCATG 847
                                                                                                                                                                                                                                                                                                         846 CATITCAGAGCIACIGAAACCAAGCAIGIGGAGCAAAAIIIGCACCAIAAICCAGGGAIIC 787
                                                                                                                                                                                                                                                                                                                                                                            966 AGCAAAGGAGAGGTAAGGATCAGACAAAGCACTAGCAACCAAGTGACCGGTGTGAGCACT 907
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|TTCCACCA 300
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Search completed: Sat Oct 23 15:30:05 1999 Job time : 3443 secs.



US-08-702-718-1.rng

Page 1



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 9.480; Variance 5.285; scale 1.794

	Pred. No.	0.00e+00	0.00+00	0.00e+00	0.00e+00	3.92e-12	5.81e-11	1.14e-09	1.14e-09	.88e-05
	Description	Potato citrate syntha 0	_	_						
SUMMARIES	ID	T03410	_		T04200 Sug			051746 011		Q70468 Gen
	Query e Match Length DB	1891 17	1891 16	1747 16	1551 16	204 1	204 1	91 9	91 9	114 12
æ	Query Match	100.0	100.0	65.5	35.1	2.3	C1	2.1	2.1	1.7
	Scor	1891	1891	1238	664	44	4.2	40	40	32
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.75e-	2.15e-04	.75e-	.75e-	.56e-0	.75e-0	.75e-0	.75e-0	.75e-0	.56e-0	.56e-0	.75e-0	.56e-0	.56e-0	.56e-0	.75e-0	.56e-0	.56e-0	.56e-0	.56e-0	.09e-0	.09e-0	.26e-0	.09e-	.26e-0	.09e-0	.09e-0	.09e-0	0-960.	ė	.256-0	.09e-	.57e-	.57e-	. 57	.57e-	
ţ,	c DNA sequenc	S	ric DNA sequen	ian DNA repl	ammalian DNA	eneric DNA se	ic	eric DNA se	C DNA S	Generic DNA sequence	C DNA S	c DNA seque	Human endothelin-1 an	Sequence encoding new	Sequence encoding new	Sequence encoding new	Sequence encoding new	nence encodin	netospiru	library	3 TSAR library	MA sequen	eneric D	Sequence encoding new	Sequence encoding new	ednence encoq	Sequence encoding new	Sequence encoding new	elope regio	an interleu	-	Human IL-8 receptor-a	Sequence encoding new	_	Sequence encoding new	
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	c 11		-									7			7	7		7		m		m	m					m						44	45	

## ALIGNMENTS

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La Cognata U, Landschutze V, Muller-Roeber B, Landschuetze V;
M PPI; 95-32153642.

The PSDB. R86383.

Inhibiting citrate synthase (CS) activity in plants - to inhibit
flower formation and improve storage capacity, e.g. in potatoes,
also new CS sense and anti-sense DNA sequences.

Claim 6; Page 15-19; 35p; German.

The potato citrate synthase (CS) gene or CDNA sequence encoding CS
(T03410) may be used to produce antisense CS sequences. CS DNA
sequences are useful for altering CS activity in plants. Antisense
CS sequences can be used to inhibit CS expression in plants and has
the effect of inhibiting flower formation and by doing so improves
the plant's storage capacity. This is partic. useful in crop plants
of any kind but esp. useful in potatoes. In addition to altering CS
                                   T03410;
24-APR-1996 (first entry)
Potato cirrate synthase gene.
Citrate synthase; inhibitor; increased storage capacity; potato;
                                                                                                                                                                                     /*tag= a
/product= potato_citrate_synthase
                                                                                                                                                                                                                                                                               09-MAR-11994; DE-4108629.
22-SEP-1994; DE-433856.
19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                  Location/Qualifiers
                   I03410 standard; cDNA; 1891 BP.
                                                                                                                                                                     ..1488
                                                                                                                                                                                                                                                             09-MAR-1994; 408629
                                                                                                             antisense DNA; ss. Solanum tuberosum.
                                                                                                                                                                                                                            DE4408629-A1.
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RESULT
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ctivity the DNA sequences can also be used to identify similar equences in the genomes of other plants and in the production of ransgenic plants with altered CS activity 425 G; 584 T; equence 1891 BP;	y Match 100.0%; Score 1891; DB 17; Length 1891; Local Similarity 100.0%; Pred. No. 0.00e+00; hes 1891; Conservative 0; Mismatches 0; Indels 0; Gap	l ttttcgttccatcagcctacttgagatgtattcccactggtaaaagttaattttttga 	61 ttttcgcgagcaatggtgttctaccgtagcgtttcgttgctgtcaaagctccgctctcga 	12  gcggtccaacagtcaaatgttagcaattctgtgcgctggcttcaagtccaaacctcttcc 	81 ggtcttgatctgcgttctgagctggtacaagaattgattcctgaacaacaggatcgcctg 	24] aaaaagatcaagtcagatatgaaaggttcaattgggaacatcacagttgatatggttctt 	301 ggtggaatgagggaatgacaggattactgtggaaacctcattaccttgaccctgatgag 	961 ggaattegetteeggggttgtetataeetgaatgeeaaaggtattaeetgeageaaag 	21 cctgggggggggccttgctgcctgaaggtcttctctggcttctttaacaggaaaggtgcca 	81   teaaaagagcaagtgaattcaattgtetcaggaattgcaggagtcgggcatcatatccetg	.41 atcatcatgtatacaactattgatgccttaccagtcacagctcatccaatgacccagttt 	.01 gctactggagtcatggctcttcaggttcaaagtgaatttcaaaggcatacgagaaaggg 	.61 attcacaaatcaaagtattgggaaccaacatatgaggattccatgaatctgattgctcaa 	21 gttccacttgttgctgcttatgtttatcgcaggatgtacaaggaatggtgacactatacct	81 aaggatgaatccctggattatggtgcaaattttgctcacatgcttggtttcagtagctct 		01 aatgicagigeteacaceggicaciiggitigetagigetiigitigicigateettaceteee
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                              961 TITGCTGCTGCTTTGAATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTT 1020
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Citrate synthase; flower formation; tuber storage; ss.
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RP PSDB: R82838.

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P-PSDB: R82838.

To improve storage of tubers, etc. and to reduce sprouting to improve storage of tubers, etc. and to reduce sprouting claim 5; Page 53-56; 87pp; English.

To identify a cDNA from potato which codes for citrate synthase, a confirmation of the complement of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos 104202 and 104203 which are complementary to the 5' or 3' end of the coding region of the arc complementary to the 5' or 3' end of the coding region of introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were uith A. thaliana citrate synthase cDNA. Positive clones were purified and sequence The nt sequence is given in 104199.

Sequence 1891 BP; 512 A; 370 C; 425 G; 584 T;
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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Mueller-roeber B;
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                                                                                                                                                                                                                                                                                                                                                                                  721 GITCCACITGITGCIGCITAIGITIAICGCAGGAIGTACAAGAAIGGTGACACIAIACCI 780
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601 GCTACTGGAGTCATGGCTCTTCAGGTTCAAAGTGAATTTCAAAAGGCATACGAGAAAGGG 660
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DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting tolaim 7: Page 60-63: 8Tpp. English.

To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solanum tuberosum citrate synthase cDNA (104199). One of the clones was sequenced. The nt. sequence is given in 704201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps 14;
                 gctggaaagttagtaatcggctgattcacgcaataaactgcaattgtgtagtttcttaaa 1860
1741 ataggtcaatgctattaatcgcgttcttggttgccattagacttgtgaatgacttccttt 1800
                                                                                                            1801 GCTGGAAAGTTAGTAATCGGCTGATTCACGCAATAAACTGCAATTGTGTAGTTTCTTAAA 1860
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Citrate synthase; flower formation;
                                                                                                                                                                                                                                                               T04201 standard; cDNA to mRNA: 1747
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22-SEP-1994; DE-435366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting Claim 6. Page 57-60; 87pp. English.

To identify a cDNA from sugar beet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepd. Plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solamum tuberosum citrate synthase cDNA (104199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is
                  1476 CAAGAAAGCATGAATTGTTTGAAATCTC-GCGAGCATAAA-CACAATGTATAATCTCTA 1533
1467 caagaaagcatgatttgtttgaaatctctgcgagcataaaagcacaatgtaaaatcttta 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 aaggtettetttggettettttaaceggaaaggtteetageaaagageaagtagatgete 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 TACAAGAATTGATTCCTGAACAACAGGATCGCCTGAAAAAGATCAAGTCAGA-TATGAAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 GATTACTGTGGAAACCTCATTACCTTGACCCTGATGAGGGAATTCGCTTCCGGGGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                  Landschutze V, Muller-rober B, Landschuetze V;
                                                                            Query Match 35.1%; Score 664; DB 16; Length 1551; Best Local Similarity 78.5%; Pred. No. 0.00e+00; Matches 997; Conservative 0; Mismatches 261; Indels 12
                                                             1527 tgaataattgcttgagaaagcagttttttttttggagc-caaggtaggtcg 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 G;
                                                                                                                                                                                25-JAN-1996 (first entry)
Sugar beet citrate synthase cDNA.
Citrate synthase; flower formation; ss.
Beta vulgaris strain Zuchtlinie 5S 0026
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 C;
                                                                                                                                            T 4
T04200 standard; cDNA to mRNA; 1551 BP.
                                                                                                                                                                                                                                                                                                                                                                                  19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHEPING AGREVO GMBH.
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Sequence 1551 BP; 455 A;
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22-SEP-1994; DE-435366
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07-MAR-1995; E00859.
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446 agactogaagogaatttoagaaggoatatgagaaagggatocataagtoaaagttttggg 505
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Base substituced E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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N81164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757 TACAAGAATGGTGACACTATACCTAAGGATGAATCCCTGGATTATGGTGCAAATTTTGCT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                        WPI; 88-279927/40.
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                   as a
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Random point muttations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to lit to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.
                                                                                                                                                                                                                                                                             E.coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the
                                                                                                                                                                                                                                         Disclosure; p; English.
Random point mutations were introduced into the alpha fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E.coli beta galactosidase alpĥa-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 Others;
                                                                                             03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 2.3%; Score 44; DB 1; Length 204; Local Similarity 6.5%; Pred. No. 3.92e-12; nes 6; Conservative 55; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Base substituted E.coli beta-galactosidase alpha-fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function=multiple cloning site 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 ccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   817 CACATGCTTGGTTTCAGTAGCTCTGAAATGCA 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 C;
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187..204
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                       /*tag=
                                                         05-MAY-1988.
30-MAR-1988; 105163.
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30-MAR-1988; 105163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also P80575.
Sequence 204 BP;
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primer_bind
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1149 TCGCAGAACTCCATGTCCAAAACCAGGGACAACCTTGCCACTGTTCAATGTTTTCCAAAC 1090
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                                                                                                                                                                                                                                      85 gymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvyn 144
                                                                                                                                                                  25 yyrcayrccbgcaggycgacbcyrraggnycccggggywccgagcycgaayycdchvgcc 84
                                                                                                                             Gaps
The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide probe MK14-A consists of nucleotides 5-95 or MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP, 5 A, 17 C, 15 G, 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide probes specific for Mycobacteria - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide probes specific for Mycobacteria - used for
                                                           108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               566 CCTTACCAGTCACAGCTCATCCAATGACCCAGTTTGCTACTGGAGTCATGGCTC 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 yvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsvctcaagcctc 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide probe MK14-A Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide probe MKÍ4-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection and amplification of Mycobacteria nucleic acid in
                                                                                            Score 42; DB 1; Length 204; Pred. No. 6.81e-11; 71; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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                                                                                                                                                                                                                                                                                                                                 1030 ICCATAGCAAAACTICCIGATIGGCIAAACCAIGAAGIGGICCG 987
                                                                                                                                                                                                                                                                                                         145 vhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv 188
                                                           11 T;
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Pred. No. 1.14e-09;
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                                                           47 C; 17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Q51746 standard; cDNA; 91 BP
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Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BECT ) BECTON DICKINSON CO.
                                                                                            Match 2.2%;
Local Similarity 16.5%;
es 27; Conservative
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Local Similarity 13.08;
                                                         21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1994 (first entry)
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26-MAY-1992; US-889651.
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26-MAY-1992; US-889651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spears PA;
                                                           204 BP;
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EP-571911-A.
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01-DEC-1993.
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                                                              Sequence
                                                                                                Query Match
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                                                                                                          δλ
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                                                                                                                                                                                                                                                                            Terbols Rolling proteins or peptide(s) which bind a ligand - by comprising a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain comprising a binding domain and an effector domain proteins comprising a binding domain and an effector forming ran also be lociclosure; page 35; 255pp; English; peptides. This generic forming can also be represented as follows: X(NNB) LICC)(NNB) & INB) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or comprising a TSAR binding domain can be used in vivo to
                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                         8 gcgssvhsyyvvhvvshhhsvhhvvhvvhhvhvvhhvvhhvhhyhvyvsvctcaa 65
                                                                                                                                                                                                                                                                                                                       114 GCGGAGCTTTGACAGCAACGAAGGTACGGTAGAACACCCATGCTCGCGAAAATCAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "this sequence_represents 'Z'; Z can be a
                                                        Oligonuclectide probe MK14.A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                            Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                   4 T;
                                                                                                                                                                                                        Score 40; DB 9; Le
Pred. No. 1.14e-09;
42; Mismatches 9
                                                                                                                                                                   15 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                               17 C;
                                         Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Q70468 standard; DNA; 114 BP
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(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                      Query Match 2.18;
Best Local Similarity 12.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q70468;
05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comments)"
                                                                                                                                                                   5 A;
                                                                                                                                                                                                                                                  7; Conservative
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WPI; 94-279739/34.
                                                                                                                                                                   91 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R65154
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01-FEB-1993;
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                                                                                                                                                                   Sequence
                       samples
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refusitiving proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a pinding domain and an effector domain.

PS Streening a recombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins.

COMPACT STATE TOWN Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be compacted as follows: X(NNB) (TGC)(NNB)12 (NNB)14 (TGC)(NNB)37. X and Y are flanking restriction sites (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in O70466-68.

COMPACTION OF TASARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and second effector peptide portion that is chancially or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed to that the expressed peptide contains 2 or 4 cysteline residues positioned in or flanking, the unpredicted or variant residues. These residues confers some degree of conformational rigidity to the peptides. The TSARs core companies, comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the company methods of hybridons demanded the end of macromolecules, eg.
                                                                                                                                                                                   943 ICIGATCCTTACCTCTCCTCTTGCTGCTGCTTTGAATGGTTTAGCCGGACCACTTCATGGT 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 GTTTCGTTGCTGTCAAAGCTCCGCTCTCGAGCGGTCCAACAGTCAAATGTTAGCAATTCT 150
                                                                                                             3 banbanbanbanbanbanbanbanbanbanbtgenabanbanbanbanbanbananna 62
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                                       Gaps
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/note= "this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
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Pred. No. 7.75e-04;
30; Mismatches 77; Indels
   Pred. No. 5.88e-05;
31; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1993: US-013416.
30-DEC-1993: US-176500.
31-JAN-1994: US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKSS DM, KAY BK;
WPI: 94-279739, PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q70465 standard; DNA; 114 BP.
Q70465;
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|larity 4.5%;
|Conservative
larity 4.5%;
Conservative
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Best Local Similarity
Best Local Similarity
Matches 5; Conserv
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0

Length 114;

DB 12;

Score 32;

1.78;

Query Match

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deliver a chemically or biologically active moiety, eg. metal ion, radiolsocope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
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                                                                                                          Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; reffector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "this sequence represents '2'; Z can be sequence of 6, 9 or 12 nucleotides (see comments)"
                      151 GIGGGTGGCTTCAAGTCCAAACCTCTTCCGGTCTTGATCTGCGTTCTGAGC 202
1.6%; Score 31; DB 12; Length 114; 3.7%; Pred. No. 2.15e-04; ative 31; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 TCATAAGAAGTTCATGCATTTCAGAGCTACTGAAACCAAGCATGTGAGC 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       direct and rapid detection in a screening process. Sequence 114\ \mathrm{BP}; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                         Location/Qualifiers
                                                                      Q70467 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                          (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 3.7%;
les 4; Conservative
                                                                                              05-APR-1995 (first entry)
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US-176500.
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WPI; 94-279739/34.
                                                                                                                                                                                                                                                                          U00977
                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R65153
                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                     01-FEB-1993;
30-DEC-1993;
                                                                                                                                                                                                                                                                                                            31-JAN-1994;
                                                                                                                                                                                                                                                 WO9418318-A
                                                                                                                                                                                                                                                             18-AUG-1994
                                                                                                                                                             Synthetic.
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                                                                                  070467;
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Matches
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\_T 12 Q70465 standard; DNA; 114

RESULT

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Disclosure; Page 35: 255pp Enquise.

Officially Page 35: 255pp Enquise.

Officially Reagents) Peptides This generate random TSAR (Totally 10765) is a generic DNA sequence used to generate formula can also be represented as follows: X(NNB) GTGO(NNB)12(NNB)14(TGO)(NNB)31. X and Y are flanking restriction sites (X is not the same as Y) that arc not specified further. Other generic sequences are shown in 707466-68.

Other specific peptides generated by these generic sequences are shown in R515-54. TSARs are concatenated heterofunctional proteins or peptides. Generated by these generic sequences are shown in 707466-68.

Offinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligourcleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in or flanking, the unpredicted or variant residues. These residues compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eq. metal ion, calloisotope, peptide, toxin or enzyme, to the specific target or on the monormal or polyclonal antibodies and therefore circumvent the need for contains and the procedic contents.
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Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                             Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening, treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35: 255pp; English.
                                                                                                                                                                                                                /*tag- a /note- "this sequence represents '2'; 2 can be a sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 1.6%; Score 30, DB 12; Local Similarity 2.0%; Pred. No. 7.75e-04;
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                                                                                                                                                      Location/Qualifiers
55..60
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                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
                      05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                         comments)"
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                                                                                                                                                                                                                                                                                                                                                                                 US-013416.
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                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1993;
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                                                                                                                                               Synthetic.
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070465;
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WHI: 94-279/3434.

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing dusion proteins or screening a recombinant vector library expressing dusion proteins.

PT comprising a binding domain and an effector domain proteins bisclosure; Page 35; 255pp; English.

CT GV469 is a generic DNA Sequence used to generate random TSAR peptide (TGC) (NNB)2(TGC) (NNB)14(TGC)Y. A and Y are flanking restriction sites (X is not the same as Y) that are not specified further. This sequence generates peptides that are cloverleaf in structure. Other of generic sequences are shown in QV465-68. Other specific peptides concatenated by these generic sequences are shown in RG5150-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically criterial regions a realise of so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues positioned in, or flanking, the conformational rigidity to the peptides. The TSARs or compone conformational rigidity to the peptides. The TSARs or compone conformational rigidity of the peptides. The TSARs or compone to in vious moiety, es, metal ion, radioisotope, peptide, toxin of a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, es, metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace of or enzyme, to the specific target or on the cell. They can also replace of conformation of macromolecules, es, monoclonal or polybridoma conformation or in vivo antibody production. The TSARs are easily detained and have designed activity allowing direct and rapid
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Mammalian DNA replication origin consensus sequence, uniorsconsensus.
DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 IGICATICCICICATICCACCAAGAACCAIAICAACTGIGAIGIICCCAAIIGAACCIII 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tgcnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                        /note= "this sequence represents 'Z'; Z can be a sequence of 6,9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 CATATCTGATCTTTTTCAGGCGATCCTGTTGTTCAGGAATCAATTCT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.6%; Score 30; DB 12; Length 114; Similarity 5.4%; Pred. No. 7.75e-04; 6; Conservative 30; Mismatches 76; Indels
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G;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection in a screening process.
Sequence 114 BP; 0 A; 4 C;
                                                                                                                                                                                                                                                                    (UYNC-) UNIV NORTH CAROLINA. Fowlkes DM, Kay BK;
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12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UYMC-) UNIV MGILL.
                                                                                                                                                                                                   01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
                     55..60
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                                                                                                                                                                                                                                                                                              Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                     misc_feature
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This sequence represents a human or mammalian DNA replication origin consensus sequences of the invention, designated uniorsconsensus.

Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into amammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned human relomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or linear, large or small yeast artificial chromosomes (YACS) or as episomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claim 1; Page 42; 54pp; English.

This sequence represents a human or mammalian DNA replication origin
consensus sequences of the invention, designated uniorsconsensus.

Administration of the consensus sequence or an anti-gene (comprising a duministration of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-1998 (first entry)
Mammalian DNA replication origin consensus sequence, uniorsconsensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 mtwaakrawrwwkkdavwwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrk 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 1.5%; Score 28; DB 46; Length 91;
Best Local Similarity 15.3%; Pred. No. 9.56e-03;
Matches 13; Conservative 46; Mismatches 25; Indels 1; Gaps
                     Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromosomes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 G;
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                                                                                                                                Claim 1; Page 42; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V44650 standard; DNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-UN-1998.
12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UYMC-) UNIV MCGILL.
WPI; 98-362770/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; ss.
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human telomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or linear, large or small yeast artificial chromosomes (YACs) or as episomal elements.
                                                                                                                                                          ·;
                                                                                                                                                                                             Query Match 1.5%; Score 29; DB 46; Length 91; Best Local Similarity 13.3%; Pred. No. 2.75e-03; Matches 10; Conservative 42; Mismatches 23; Indels 0; Gaps
                                                                          4 G;
                                                                          1 C;
                                                                          Sequence 91 BP; 15 A;
86666
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Search completed: Sat Oct 23 16:31:37 1999 Job time : 429 secs.

Cp 1492 CAATTCATGCTTTCT 1478 73 atakwwwkdakwkmw 87

qq

Page 1

(MT)
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn MasPar time 136.79 Seconds 1195.578 Million cell updates/sec Run on:

Sat Oct 23 16:31:55 1999;

Tabular output not generated.

>US-08-702-718-1 (1-1891) from US08702718.seq 1891 Description: Perfect Score: Title:

N.A. Sequence: Comp:

Scoring table:

TABLE default Gap 6

165359 seqs, 43243793 bases x 2 Searched:

Dbase 0; Query 0

STD

Nmatch

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 9.032; Variance 4.359; scale 2.067

Statistics:

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
0	45	4.	7218	C1	US-08-232-	Sequence 14, Applicati	4.04e-16
7	4.2	ci ci	7218	N	US-08-232-	Sequence 14, Applicati	5.99e-14
m	34	1.8	965	٣	US-08-388-	22,	2.31e-08
4	31	1.6	215	7	US-08-238-	5, A	2
c S	31	1.6	215	٦	US-08-238-	Sequence 5, Applicatio	~
9 0	28	1.5	965	ĸ	US-08-388-	22	1.95e-04
7	28	1.5	1302	ĸ	US-08-529-		ä
۵ د	26	1.4	7.4	4	PCT-US95-1	10	3.40e-03
6 0	26	1.4	81	4	PCT-US95-1	98,	3.40e-03
10	24	1.3	75	4	PCT-US95-1	66	5.36e-02
11	24	1.3	81	4	PCT-US95-1	92,	5.36e-02
12	24	1.3	82	4	PCT-US95-1	Sequence 97, Applicati	5.36e-02
13	24	1.3	93	٣	US-08-353-	16,	5.36e-02
14	24	1.3	105	Н	us-07-865-	Sequence 13, Applicati	5.36e-02
15	25	1.3	195	٣	US-08-137-	7, 4	1.37e-02
c 16	23	1.2		П	US-08-471-	Sequence 145, Applicat	2.04e-03
c 17	23	1.2	68	П	US-08-471-	143,	2.04e-01
18	22	1.2	74	4	PCT-US95-1	94, A	7.54e-01
c 19	22	1.2	75	4	PCT-US95-1	66	7.54e-01
c 20	22	C:	c: oc	4	PCT-US95-1	0.7	7.546-01

2.04e-01 7.54e-01 7.54e-01 7.54e-01			2.69e+00 2.69e+00 2.69e+00 2.69e+00 2.69e+00 2.69e+00 2.69e+00
Sequence 16, Applicati Sequence 13, Applicati Sequence 2, Applicatio Sequence 2, Applicatio	1, 28, 28,	24, 15, 15, 15, 15, 15, 15, 15, 15, 15, 15	3, 12, 12, 2,
-353- -865- -357- -878-		US-08-676- Sequence of the control o	5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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92 105 108	242 1812 1812 1812 1812 1978	2277 2277 547 699 748 242	786 840 840 840 940 1408 1608
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Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. S670360
Sequence 14, Application US/08232463
Patent No. S670360
SEGENELLOAT:
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: ALACADERS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTR: USA
CONTRES: TANANDRIE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 38472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEPAX: (903)683-4109 TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
  T. 1. US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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                                                                                                                                                                                  457 GITAAAARAAAGGAAGAAGAGCITCAGGGAAGGGGICACGCCCAGGCITIGCIGCAGGT 408
                                                                                                                                                                                                                        407 AATACCITTTGGCATTCAGGTATAGACCAACCCCGAAGCGAATTCCCTCATCAGGTCCA 348
                                                                                                                                                                                                                                                                347 AGGTAATGAGGTTTCCACAGTAATCGTGTCATTCCTCTCTTTCCACTAGAACCATATCA 288
                                                                                                                                                                                                                                                                                                       287 ACTGIGATGTICCCAATIGAACCITICATATCIGACITGATCTTTTTCAGGCGAICCTGT 228
                                                                                                    Gaps
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                                               CLONE: pT29pt-FIs
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                              2.4%; Score 45; DB 2; Length 7218; Similarity 1.8%; Pred. No. 4.04e-16; 6; Conservative 179; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F. APPLICANT: APPLICANT: RALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY 6 Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                           JT 2
US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-406-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                           1416 YYYYYYYYYYYYYYYYYYYYYY 1440
                                                                                                                                                                                                                                                                                                                                               227 IGTICAGGAATCAATTCTTGTACCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PPIOR APPLICATION DATA:
                             linear
                                     IMMEDIATE SOURCE:
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                             TOPOLOGY:
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 LENGIH:
                                                                                Query Match
                                                                                                   Matches
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61 ITITICGCGAGCAATGGTGTTCTAGCGTTTGGTTGGTGTGAAAGGTGGGGTGTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TITITGGIICCATCAGCCIACTIGAGAIGIATICCCACIGGIAAAAGITAATTTTTGA 60
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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IMMEDIATE SOURCE:
CLONE: pT22pt-F1s
SEQUENCE 7218 FP: 1944 A, 1491 C, 148G G, 1929 T, 368 OTHER.
                                                                                                                                                                                                                                                                                                                                         2.2%, Score 42, DB 2, Length 7218; Similarity 1.9%, Pred. No. 5.99e-14; 4; Conservative 121; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carr, Frank J.
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Welt, Sydney
TITLE OF INVENTION: Recombinant Human Anti-Lewis B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
RECISTRATION NUMBER: 29,768
REPERIOR/COCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-388-672A-22 STANDARD, DNA, UNC; 965 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/388,672A
14-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GGTCTTGATCTGCGTTCTGAGCTGGTAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ď.
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NAME: Hanson, NO. 5795961man
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wallace, T. Paul
Harris, William J.
                                                                                            TELES: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Felfe and Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 14-FEB-199
CLASSIFICATION:
                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               Query Match
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Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569930
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: BENNETT, Alan
APPLICANT: DOWELL, Ann
APPLICANT: TOTAL, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       129 SRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSN 188
                                                                                                                                                                                            69 GGNNVGAAKTHYYTHINVSGADSKTVIDSYNASGISSSNGGIDGNRSGADSYGSSKTAMT 128
                                                                                                                                     9 SSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNY 68
                                                                                                         1; Gaps
                  /standard_name= "Deduced amino acid
                                                                         Score 31; DB 1; Length 215;
Pred. No. 2.30e-06;
75; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
   LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amir OTHER INFORMATION: sequence of PGIP from bean." SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BASTIAN, Kevin L.
REGISTATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           1146 GCGAAAGACTGTACCAAGAT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                              189 VSNNCGGGNKRDVSSYANNK 208
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                         Query Match 1.6%;
Best Local Similarity 14.0%;
Matches 28; Conservative
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unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH,
APPLICANT: POWELL, Ann
APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                       1400 TAATTTGGGACCGAGCTCTTGGATTGCCGCTAGAGAGGCCAAAGAGTGTCACAATGGAGT 1459
                                                                                                                                                                                                                                                   851 TAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSSTTHGNGN 910
                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                         Score 34; DB 3; Length 965; Pred. No. 2.31e-08; 42; Mismatches 25; Indels
                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                      T 4
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP
REFERENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LEGITH: 965 base pairs
TYPE: nucleic acid
STRENDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5: SEGUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                               1460 GGCTTGAGAACCAGTGCAAGA 1480
                                                                                                                                                                                                                                                                                                           911 TYYWYKGKAKYRVSNRSGVSR 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                            1.8%;
                                                                                                                                                                                                       Best Local Similarity 17.3%;
Matches 14; Conservative
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ZIP: 94105-1493
                                                                                                                                                                                            Query Match
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SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER

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121 GSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNR 180
                                                                                                                                                                    291 ATCAACTGTGTTGCCCAATTGAAGCTTTGATATCTGACTTGATCTTTTTCAGGCGATC 232
                                                                                                                                                                                                   61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSY 120
                                                                                                                                                                                                                                231 CTGTTGTTCAGGAATCAAATTCTTGTACCAGCTCAGAACGCAGATCAAGACCGGAAGAGGT 172
                                                                                                                                                                                                                                                                                            171 TIGGACTIGAAGCCAGCGACAGAATIGCIAACATIIGACIGIIGGACCGCTCGAGAGCG 112
                                                                                                                                      1 MINVIMSSSSVVSRIASCNDKAKKDGNIISSWIIDCCNRIWGVCDIDIIYRVNNDSGHNK 60
                                                                                                        0; Gaps
         OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                        80; Mismatches 104; Indels
                                                                       Score 31; DB 1; Length 215, Pred. No. 2.30e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wallace, T. Paul
APPLICANT: Wallace, T. Paul
APPLICANT: Garr, Frank J.
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Recombinant Human Anti-Lewis B
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-388-672A-22 STANDARD; DNA; UNC; 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/388,672A FILING DATE: 14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, NO. 5795961man D. REGISTRATION NUMBER: 30,946
RESERENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION-
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         181 YGTGTKSNVSNNCGGGNKRDVSSYANNK 208
                                                                                                                                                                                                                                                                                                                                                      111 GAGCTTTGACAGCAACGAAACGCTACGG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Felfe and Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                          Query Match 1.6%;
Best Local Similarity 11.5%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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 LOCATION: 1..215
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5795961
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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1589 AAGGGCCGACCTAICTIGTCCCCCAAGAAAGGAGIGCTTIGICAAGCAATTAITCATAGA 1530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1706 AAIICCIC-ACACGCIGAICCAGCAIGTAAAAAITAATAGGICAAIGCIATTAATCGCGI 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754 CNCARMGNGAYATGYINYTNAARMGNGCNCARCCNATHGGNWSNGTNYTNYTNATGGTNT 823
                                                                      836 ADTSSNSRSSVTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGD 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                704 INTINGAYYINWSNCCNGCNTAYGGNGCNTTYYTNGGNGGNGINGINYTNGGNAAYWSNG 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PROTEIN BOUND MAGNETIC PARTICLES AND TITLE OF INVENTION: PROCESS OF PRODUCING THE SAME NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: PILLSBURY MADISON & SUIRO, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 1302; Score 28; DB 3; Length 1302; Local Similarity 32.2%; Pred. No. 1.95e-04; nes 49; Conservative 26; Mismatches 76; Indels
Score 28; DB 3; Length 965; Pred. No. 1.95e-04; 38; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 1302 BP; 143 A; 118 C; 259 G; 216 T; 566 OTHER.
                                                                                                                                                                                                                                               US-08-529-600D-3 STANDARD; DNA; UNC; 1302 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 TYTTYYTNWSNATHGGNYTNYTNYTNGAYTTY 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,600D
FILING DATE: 18-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                           1529 GATTATACATTGTGTTTTATGCTCGCGAG 1501
                                                                                                                                          896 RVTTCRSSTTHGNGNTYYWYKGKAKYRVS 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-248700
FILING DATE: 16-SEP-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08529600D Sequence 3, Application US/08529600D Patent No. 5861285
                                                                                                                                                                                                                                                                                                                                                                       Tadashi MATSUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1302 base pairs
Query Match 1.5%;
Best Local Similarity 21.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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RESULT

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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           901 TACCAC 896
                                                                                                                                                                                                                                                                                                                                         72 NACCAC 77
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                                                                                                                                                                                                                                                                                                                                                                                                           XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                       APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennia & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.4%; Score 26; DB 4; Length 74; Best Local Similarity 9.1%; Pred. No. 3.40e-03; Matches 6; Conservative 20; Mismatches 40; Indels
                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP: 6 A: 6 C: 1 G: 1 T: 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .T
PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                1101-196-228
PCT-US95-11934-100 STANDARD; DNA; UNC; 74
                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                            Sequence 100, Application PC/TUS9511934 Sequence 100, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1101-:
TELECOMOVINGATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARRATERISTICS:
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
New York
                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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STATE: Ne
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COMPUTER READLE FORM:

WEDINY TYPE: Flopp disk

COMPUTER: IRM PC COMPATION:

WEDINY TYPE: Flopp disk

COMPUTER: IRM PC COMPATION:

CLASSTRANDELL NATURE NUMBER:

WEDINY TYPE: MARKED AND STREET 10, Version #1.30

CLASSTRANDELL NATURE NUMBER:

WARTHER MARKED AND STREET 10, Version #1.30

CLASSTRANDELL NATURE NUMBER:

REGISTRANDER OF SERVICE NUMBER:

REGISTRANDER NUMBER:

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                                                                                                                                                                                                                            CITY: N
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                                                                                                                                                                           907 AGTGCTCACACCGGTCACTTGGTTGCTAGTGCTTTGTCTGATCCTTACCTCTCTTTGCT 966
                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103
                                                                                                             Ouery Match 1.3%; Score 24; DB 4; Length 75; Best Local Similarity 7.5%; Pred. No. 5.36e-02; Matches 5; Conservative 20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vuely Match 1.3%; Score 24; DB 4; Length 81; Best Local Similarity 17.1%; Pred. No. 5.36e-02; Matches 13; Conservative 16; Mismatcher 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                 T 11
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                     Sequence 92, Application PC/TUS9511934 Sequence 92, Application PC/TUS9511934 GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEFAX (212) 869-9741/8964
TELEX: 66141 PENNTE
INFORMATION FOR SEQ 1D NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH. 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORREY/AGENT INCORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION UNDRER: 18,872
PEFFRATION INTORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                      New York
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                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                  967 GCTGCTT 973
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                               64 NNBGGTT 70
                                                                                                                                                                                                                                                                                                                                                                                             CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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907 AGIGCICACACCGGICACIIGGIIGCIAGIGCIIIIGICIGAICCIIACCICICCIIIIGI 966
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                                                                                                                                                                                                                                                              Sequence 97, Application PC/TUS9511934
Sequence 97 Application PC/TUS9511934
GENERAL INFORMATION:
APPLICART: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 24; DB 4; Length 82; 7.5%; Pred. No. 5.36e.02; ative 20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-353-372A-16 STANDARD; DNA; UNC; 92 BP.
                                                                                                                                                                              JT 12
PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SE: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08353372A Sequence 16, Application US/08353372A Patent No. 5840479 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                            1704 CGAATTCCTCACACGC 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 7.5%;
Matches 5; Conservative
                                                               63 NBNNBNNBNACGC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCETAGE
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APPLICANT: Marcia M. Miller
TITLE OF INVENTION: Restriction Fragment Length
TITLE OF INVENTION: Polymorphism Test For Haplotyping Domesticated Fowl
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 CAAAGCCTGGGGGTGAGCCCTTGCCTGAAGGTCTTCTCTGGGCTTCTTTTAACAGGAAAGG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 SNNNKSNNAVKNGNNAKNSGKNKSANAVNNGNNAKNSNNNKSNNMGTPDMKNNRNAAKNN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 1; Length 105;
Pred. No. 5.36e-02;
27; Mismatches 53; Indels
                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 3M Double Density 5 1/4" diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRIGINAL SOURCE: Synthetically Prepared IMMEDIATE SOURCE: Synthetically Prepared SEQUENCE 105 BP; 15 A; 0 C; 8 G; 1 T; 81 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .r 15
US-08-137-175A-7 STANDARD; DNA; UNC; 1958 BP.
                                                                                                                                                                                                                                               COMPUTER: Wang PC
OPERATING SYSTEM: MS DOS Version 3.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5451670e
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/865,662F
FILING DATE: 07 April, 1992
CLASSIFFCATION: 435
PRICE APPLICATION DATA:
APPLICATION NUMBER: 07/688,926
FILING DATE: 22 April 1991
APPLICATION NUMBER: 07/210,405
FILING DATE: 23 June 1988
APPLICATION NUMBER: 07/210,405
FILING DATE: 23 June 1987
APPLICATION NUMBER: US 07/130,529
FILING DATE: 9 December 1987
APPLICATION NUMBER: US 07/130,529
FILING DATE: 30 June 1987
APPLICATION NUMBER: US 07/100,529
FILING DATE: 30 June 1987
                                                                                                        STATE: 1900 CITY: Duarte STATE: California COUNTRY: United States of America 21P: 91010-0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 NSGVADNKNNASNNYDNGSGVADNKNAAKNNY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 IGCCAICAAAAGAGCAAGIGAAIICAAIIGIC 507
                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,662F
FILING DATE: 07 April, 1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/068,176
FILING DATE: 30 June 1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08137175A Sequence 7, Application US/08137175A Patent No. 5777095 GENERAL INFORMATION: APPLICANT: BERBGSTROEM, Alan G. APPLICANT: BERBGSTROEM, Sven
                                                                                                    ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: NO.
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
TELEFIX: (0.5 451670e
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.3%;
Best Local Similarity 13.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 105
TYPE: Nucleic Acid
STRANDEDNESS. Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: D
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXXX
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         á
                                                                                            TITLE OF INVENTION: Preparation and Use of Gene Banks of
TITLE OF INVENTION: Synthetic Human Antibodies ("Synthetic Human-Antibody
TITLE OF INVENTION: Libraries")
NUMBER OF SEQUENCES: 39
COPPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Pred. No. 5.36e-02;
24; Mismatches 13; Indels
                                                                                                                                                                                            Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,372A
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
FILING DATE: 23-MAY-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 BAKCHNBHHKNNBRPTPPCPVTAHARVMTATPVCSMMAVMBTCVD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
SEQUENCE 92 BF; 13 A; 10 C; 17 G; 17 T, 35 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05552.1032-02000
                                                                                                                                                                                                                               STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 02 897.6
FILING DATE: 01-FEB-1990
PRIOR APPLICATION DATE: APPLICATION NUMBER: DE P 40 03 880.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE P 40 03 880.7
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .T 14
US-07-865-662F-13 STANDARD; DNA; UNC; 105
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Sequence 13, Application US/0786562F
Patent No. 5451670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07/654,207
APPLICANT: Little, Melvyn
APPLICANT: Breitling, Frank B
APPLICANT: Seehaus, Thomas
APPLICANT: Dubel, Stefan
APPLICANT: Klewinghaus, Iris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FORMan, David S.
REGISTRATION NUMBER: 33,694
PEFERENCE/POCKET NUMBER: 055
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION.
PRIOR APPLICATION NUMBER: 07/654
APPLICATION NUMBER: 07/654
FILING DATE: 30-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 92 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.3%;
Best Local Similarity 17.8%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                  Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                     STATE:
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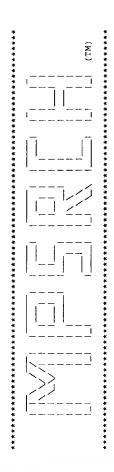
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Gaps
APPLICANT: HANSSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolate from I. persulcatus from Soviet Union
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                  COMPUTER EAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,175A
FILING DATE: 26-OCT-1993
CLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYEE P.
NAME: COOPER, IYEE P.
REGISTRATION NUMBER: 28.005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 959.1843
OTHER INFORMATION: /product- "OspB"
SEQUENCE 1958 BP, 837 A; 284 C, 340 G, 497 T, 0 OTHER.
                                                                    ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY USA
21P: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.3%; Score 25; DB 3; Len Best Local Similarity 83.8%; Pred. No. 1.37e-02; Matches 31; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1852 TTTCTTAAATTTGCTAATTCTTATTTGATGATATTAT 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 TITITITAATITGCIATITGTTATITGTIGATCITAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 125..949
OTHER INFORMATION: /product- "Ospa"
                                                                                                                                                                                                                                                                                                                                                                          BARBOUR-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Sat Oct 23 16:34:16 1999 Job time: 141 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Borrelia burgdorferi
STRAIN: Ip90
INDIVIDUAL ISOLATE: Isolate fro
INDIVIDUAL ISOLATE: Soviet Unit
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE DOCKET UNMER:
REFERENCE DOCKET UNMER:
TELECOMMUNICATION INFORMATION:
TELEFAN:
TELEFAN:
TELEFAN:
TELEX:
202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE:
 qq
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US-08-702-718-2.rai



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:36:55 1999; MasPar time 7.33 Seconds 752.832 Million cell updates/sec Run on:

Title:

Tabular output not generated.

>US-08-702-718-2 (1-471) from USO8702718.pep 3466 1 MVFYRSVSLLSKLRSRAVQQ......PLERPKSVTMEWLENOCKKA 471 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

119857 segs, 11713122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Mean 33.654; Variance 162.896; scale 0.207 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	No.	42e+00	.42e+00	.77e+00	79e+01	80e+01	80e+01	80e+01	85e+01	85e+01	05e+01	.36e+01	85e+01	85e+01	04e+01	e+01	77e+01	77e+01		04e+31	04e+01 39e+02	000	.04e+01 .39e+02 .60e+02 .20e+02	04e+01 39e+02 60e+02 20e+02 60e+02
	pred.	2.42	2.42	1.77	1.79	2.80	2.80	2.80	5.85	Ŋ.	S.	4	5	5.85	9.04	7.82e+0	6.77	6.77		9.04				
	Description		10,	2,2		Sequence 5, Applicatio	5,	'n	23	10	12	'n	7	7		Sequence 4, Applicatio	7	148	,	000	, , ,	જે તે તે	ย์ก่อ	, i i i i i i i i
	ID	US-08-063-	PCT-US93-0	ns-07-689-	5320958-6	US-08-450-	PCT-US95-0	0-80-	US-08-245-	US-08-245-	US-08-637-	US-08-844-	US-08-463-	9	5320958-2	US-08-742-	US-08-742-	US-08-592-	TIS-08-149-		US-08-818-	-08-818 -08-761	-08-818 -08-761 -08-933	-08-818 -08-761 -08-933
	DB	-	m		4	_	m	1	C3	C ŧ	7	-	7	7	4	C1	7	7	c		7	(7) (3)	010101	9000
	Length	220	220	3031	268	355		355	96	108	225	587	1548	1548	485	763	771	1312	2265		7	170 335	170 335 340	170 335 340 509
æ	Query Match	3.3	3.3	3.3	2.9	2.8	2.8	2.8	2.7	2.7	2.7	2.7	2.7	2.7	5.6	5.6		٠						นเนเน พพพพพ
	Score	113	113	115	100	97	97	97	92	35	93	94	92	92	68	06	91	91	68		86	8 8 8 5	86 85 87	88 83 83 83
	Result No.	-	2	3	4	S	φ	7	80	თ	10	11	12	13	14	15	16	17	18		19	19	19 20 21	15 15 15 15 15 15 15 15 15 15 15 15 15 1

86 2.5 572 2 US-08-745- Sequence 1, Applicatio 1.39e+02 85 2.5 668 1 US-08-205- Sequence 2, Applicatio 1.39e+02 86 2.5 668 1 US-07-891- Sequence 2, Applicatio 1.39e+02 87 2.5 1147 2 US-08-35- Sequence 3, Applicatio 1.39e-02 87 2.5 1147 2 US-08-135- Sequence 3, Applicatio 1.20e-02 87 2.5 1147 1 US-08-144- Sequence 3, Applicatio 1.20e-02 87 2.5 1165 2 US-08-135- Sequence 2, Applicatio 1.20e-02 87 2.5 1165 2 US-08-135- Sequence 3, Applicatio 1.20e-02 87 2.5 1165 2 US-08-135- Sequence 3, Applicatio 1.20e-02 88 2.4 114 2 US-08-149- Sequence 3, Applicatio 1.20e-02 83 2.4 114 2 US-08-149- Sequence 3, Applicatio 1.20e-02 83 2.4 114 2 US-08-149- Sequence 3, Applicatio 1.20e-02 83 2.4 114 2 US-08-149- Sequence 3, Applicatio 2.12e-02 84 2.4 230 2 US-08-67- Sequence 25, Applicatio 2.12e-02 84 2.4 230 2 US-08-67- Sequence 25, Applicatio 2.12e-02 84 2.4 317 1 US-08-95- Sequence 25, Applicatio 1.84e-02 84 2.4 312 US-08-95- Sequence 2, Applicatio 1.84e-02 84 2.4 312 US-08-95- Sequence 2, Applicatio 2.12e-02 83 2.4 1367 2 US-08-49- Sequence 2, Applicatio 2.12e-02 83 2.4 1367 2 US-08-84- Sequence 2, Applicatio 2.12e-02 15-	Sequence 10, Application US/08063552 Sequence 10, Application US/08063552 Patent No. 568936 CENERAL INFORMATION: APPLICANT: ECWards, Robert H TITLE OF UNEWRION: Vesicle Membrane Transport Proteins NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSE: Sheldon & MAK STREET: 225 South Lake Avenue, Ninth Floor CITY: Pasadena STREET: 221 South Lake Avenue, Ninth Floor CITY: Pasadena STREET: California COUNTRY: USA COUNTRY: USA COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-DOS SOFTWARE: PATENT NORPATION: MEDIOM TYPE: PATENT NORPATION: MEDIOM TYPE: PATENT NOR VORBATION: APPLICATION NUMBER: US 2004 NOS 352 CURREDT INFORMATION: RESISTRATION NUMBER: 32,612 RESERBENCE/DOCKET NUMBER: 32,612 RESERBENCE/DOCKET NUMBER: 32,612 RESERBENCE/DOCKET NUMBER: 32,612 RESERBENCE/DOCKET NUMBER: 32,613 RESERBENCE/DOCKET NUMBER: 32,613 RESERBENCE/DOCKET NUMBER: 32,613 RESISTRATION NUMBER: 32,613 RECOMMUNICATION INFORMATION: TELEPHONE: (818) 796-6310 TELEPHONE: (818) 796-6310 TELEPHONE: (818) 796-631 INFORMATION FOR SEQ 1D NO: 10: SEQUENCE HARACTERERICE: 10 NO: 10: SEQUENCE HARACTERERICE: 10 NO: 10: SEQUENCE HARACTERE SITEME NO NUMBER: 120 main orids TOPOLOGY: 11 noar MULECULE TYPE: AMINO ACID TYPE: AMINO
25 25 26 26 27 28 33 33 33 33 34 34 35 36 37 44 42 44 45 45 46 46 47 47 47 48 48 48 48 48 48 48 48 48 48 48 48 48	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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84 VGPLTNRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
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                                                                                       209 DSMNLIAQVPLVAAYVYRRMYKNGDT-IPKDESLDYGANFAHM-LGFSSSEMHELLMRLY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 DSMNLIAQVPLVAAYVYRRMYKNGDT-IPKDESLDYGANFAHM-LGFSSSEMHELLMRLY 266
                                                                    24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
                                                  Gaps
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                                                                                                                                                                                                                                                            GENEFAL INFORMATION:
APPLICANT: Edwards, Robert H
TITLE OF INVENTION: Vesicle Membrane Transport Proteins
NUMBER OF SEQUENCES: 17
                                                                                                                         267 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.3%; Score 113; DB 3; Length 220; Best Local Similarity 20.2%; Pred. No. 2.42e+00; Matches 22; Conservative 41; Mismatches 41; Indels
                             Length 220;
                                                                                                           84 VCPLTNRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
                           7. Match 3.3%; Score 113; DB 1; Length 220; Local Similarity 20.2%; Pred. No. 2.42e+00; Des 22; Conservative 41; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING NATE:
                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                   CORPESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Max
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                       220
                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: PCT/US93/05704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9067-1PCT
                                                                                                                                                                       PRT;
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220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                                    Sequence 10, Application PC/TUS9305704
NISM: Rattus rattus
220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                 Sequence 10, Application PC/TUS9305704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 220 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO FRANCES
                                                                                                                                                                                                                                                                                                                       STREET: 225 South
CITY: Pasadena
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                     PCT-US93-05704-10
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ORGANI SM:
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        SEQUENCE
                             Query Match
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                                                Matches
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420 PLAFLFFGQNIIAASPLAVLAYAIPHMFHSIATA-AKV-NKG-WRYSFWSEVYETTMALF 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wong, Hing
APPLICANT: Benziman, Moshe
TITLE OF INVENTION: METHODS AND NUCLEIC ACID SEQUENCES FOR THE
TITLE OF INVENTION: EXPRESSION OF CELLULOSE SYNTHASE OPERON
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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267 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5: McCutchen, Doyle, Brown & Enersen
Three Embarcadero Center
                                                                                                3031 AA
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JENCE 3031 AA, 328497 MW; 44365167 CN;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 337,194
FILING DATE: 12-ARP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 96,236
FILING DATE: 23-MAR-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
                                                                                              PRT;
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MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07689008
Patent No. 5268274
                                                                                                                                                                                                                                         Sequence 2, Application US/07689008
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REGISTRATION NUMBER: 31547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Ben-Bassat, Arie
Calhoon, Roger D
                                                                                                                                                                                                                                                                                                                                                                                                                              Gelfand, David H
Meade, James H
Tal, Rony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 393-2000
TELEFAX: (415) 393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 340817 MACPAG SFO INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Fear, Anna L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Three Embarc
CITY: San Francisco
STATE: California
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TOPOLOGY: 11nes
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                                                                                              US-07-689-008-2
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APPLICANT:
APPLICANT:
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APPLICANT:
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477 LVRVTIITLMFPSKGKFNVTEKGGVLEEEFFDLGATYPNII-FAGIMTLGLLIGLFELTF 535
                                                                                                                                                                                                                                                                                                                35 KAAQRWVLSNVVERLPVHGAAHGFVAGRSILTNALAHQGADVVVKVDLKDFFPSVTWRRV 94
                                                                                                                                                                                                                                                                                                                          16 RAVQQSNVSNSVRWLQVQTSS-GL-DLRSELVQELIPEQQDRLKKIK-SDMKGSIGNITV 72
                                                                                                                                                                                                                                                                                               9; Gaps
                                                                                                                                                                        APPLICANT: INOUYE, SUNIKO; HSU, MEI-YIN; EAGLE, SUSAN; INOUYE, MASAYORI
TITLE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASE NUMBER OF SEQUENCES: 24 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/315,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                           Score 100; DB 4; Length 268; Pred. No. 1.79e+01; 25; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          355 AA
                                                                                         290 AA
                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/315,316
FILING DATE: 24-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                          290 AA; 32072 MW; 450220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08450393A
                                                                                         PRT;
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ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                           Match 2.9%;
Local Similarity 29.2%;
Les 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                          STANDARD;
                                                                                                                                                Patent No. 5320958.
                                                                                                                                                                 5320958
                                                                                                                                                                                                                                                 LENGTH: 268
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US-08-450-393A-5
                                    536 HFNQLAG 542
                                                      270 HSDHEGG 276
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                                                                                                                                                                                                                                         SEQ ID NO:6
                                                                                                                             01-JAN-1900
                                                                                                                                                                   Patent No.
                                                                                        5320958-6
                                                                                                                                                                                                                                                          SEQUENCE
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65 LKNMTSIYLLNLAISDLLFLFTLPFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS NUMBER OF SOUTHOUSS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 2.8%; Score 97; DB 1; Length 355; Local Similarity 31.9%; Pred. No. 2.80e+01; nes 23; Conservative 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Robbins, Berliner & Carson
201 N. Figueroa Street, 5th Floor
                                                                                                                                          UCAL-237/02US
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NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERNCE/DOCKET NUMBER: 5555-291
TELECOMMINICATION INFORMATION:
TELEPHONE: 310-977-1003
APPLICATION NUMBER: US/08/450,393A FILING DATE: MAY 25, 1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application PC/TUS9500476
                                                                                                            REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-843-5165
TELEFAX: 415-8857-0663
TELEFAX: 380816CO01eyPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins,
                                                                                                Cserr, Luann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 IILLTIDRYLAI 135
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23; Conservative 14; Mismatches 29; Indels
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IMMEDIATE SOURCE:
                                                                                                                                                                         124 IILLTIDRYLAI 135
                                                                                                                                                                                                                                 428 TVLFGVSRALGI 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>0</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07601
                                                                                                                                                                                                                                                                                                                                                   US-08-245-511-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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TITLE OF INVENTION: Cloning and Expression of Human

TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1

TITLE OF INVENTION: alpha)/RANTES Receptor

NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                 65 LKNMTSIYLLNLAISDLLFLFTLPFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend Khourle and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                        Score 97; DB 3; Length 355; Pred. No. 2.80e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.8%; Score 97; DB 1; Length 355; Best Local Similarity 31.9%; Pred. No. 2.80e+01;
                                                                                                                                                                                                                                                                                                                                                   14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Weber, Kenneth A.
REGISTPATION NUMBER: 31,577
TERERENCE/FOCKET WMBER: 15280-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                    355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08012988A Patent No. 5652133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08012988A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                    LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-543-5043
                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                        y Match
Local Similarity 31.9%;
hes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 199301;
CLASSIFICATION: 435
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                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                            Query Match
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373 MKHLPEDPLEQL-VSKLYEVFLL-FLQNLAKLKP-WPNVDAHSGVLLN-YY-GLTEARXY 427
                                          65 LKNWTSIYLLNLAISDLLFTEFTEFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29, Application US/08245511
Patent No. 5928900
GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: RACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: US/08/245,511
FILING DATE: WAY-1994
CLASSIFICATION: 4.24
PRICA APPLICATION NUMBER: US 08/116,541
FILING DATE: 01.5EP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        98 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: SPRU87
98 AA; 10496 MW; 48418 CN;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/08245511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REPERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internal
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
: USA
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87 IIPETLPSQM 96 | : : | 70 ITVDMVLGGM 79

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LSKLRSRAVQQSNVSNSVPWLQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIGN 69
Best Local Similarity 24.3%; Pred. No. 5.85e+01;
Matches 17; Conservative 20; Mismatches 31; Indels 2; Gaps
                                         26 MTRLRVTVKDADKVGNAEQW-KAEGAMGLVMKGQGVQAIYGPKADILKSDIQDILDS-GE 83
                                                          10 LSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Caps
                                                                                                                                                                                                                                                                                                                          APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tromanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 92; DB 2; Length 108;
Pred. No. 5.85e+01;
20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                            108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
PEGISTPATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
HENCE 108 AA; 11664 MW; 59621 CN;
                                                                                                                                                                                                                                                                                Sequence 10, Application US/08245511
Patent No. 5928900
GENERAL INFORMATION:
APPLICANT: Masure, H Robert
                                                                                                                                                                                                                                                                                                                                                                                                                        E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                          Sequence 10, Application US/08245511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.7%;
Best Local Similarity 24.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                            84 IIPETLPSOM 93
                                                                                                              70 ITVDMVLGGM 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                           US-08-245-511-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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366 TCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYYGLTEAR 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 2; Length 225; Pred. No. 5.05e+01; 24; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY 1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: PCT/GB95/02875
ATTORNEY/AGBNT INFORMATION:
NAME: PADSE, PATICAL I.
             225 AA.
                                                                                                        Sequence 127, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
                                                                                                                                                                                                                                                       STAIL:
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--wertter: IBM PC compatible
--wertter: IBM PC compatible
--wertter: TRM: PC DOS/MS-DOS
             FRT;
                                                                                                                                                                                                   ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AA; 25356 MW; 275619 CN;
                                                                                      Sequence 127, Application US/08637759B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: RPI
TELECOMMUNICATION INFORMATION:
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 225 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.7%;
Best Local Similarity 23.0%;
Matches 17; Conservative
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 YYTVLFGVSRALGI 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PNIALYGLALVLSL 74
                                                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
          US-08-637-759B-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                       XXXXXX
RESULT
ID US
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587 AA.

STANDARD;

JT 11 US-08-844-280-2

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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 1548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.7%;
Best Local Similarity 28.2%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 GWEPVFLARIQDARSREL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 LWKPHYLDPDEGIRFRGL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                  CITY: Kingston
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-460-907B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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76 LGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECGKVLPAAKPGGEPLPEGLLWLLLTGKV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 VGRRRDLGGLIFI-D-LRDREGIM-Q-LVI-NPEKVSAEVMATAESLRSEFV-IEVTGQV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.7%; Score 94; DB 1; Length 587; 28.4%; Pred. No. 4.36e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1548 AA.
                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: FILING DATA:
                                                                                GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5747315el Compounds
                                                                                                                                 ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                          томыЕR: US/08/844,280
18-APR-1997
N:
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P31457-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 587 AA; 66220 MW; 1692397 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                  CLASSIFICATION: ?
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 9607993.4
FILING DATE: 18 APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08463092B Patent No. 5766880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 AAREQANDKLPTGAVELNVTALIVLNTA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 PSKEQVNS-IVSGIAESGIISLIIMYTT 162
                                                                Sequence 2, Application US/08844280 Patent No. 5747315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08463092B
                                              Sequence 2, Application US/08844280
                                                                                                                                                                                                                                                                                                                            38,891
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                     1: 587 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHAPACTERISTICS
                                                                                                                                                                     COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                              NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 28.4%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                             STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-463-092B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
          XXXXXX
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370 VGWLRVPGMAVLFVTLPL-QAVISKHVQDVSERMASVVDLRI-KRINEL-LSGVRIVKFM 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92, DB 2, Length 1548,
Pred. No. 5.85e+01;
18; Mismatches 34; Indels 4; Gaps
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 1548 AA; 172282 MW; 12743552 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOP APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-007-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
                                                                                                                                                                                                                                                                      COUNTRY: CAMBA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: Q1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
```

525 AA.

PRT;

STANDARD;

5320958-2

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370 VGWLRVPGMAVLFVTLPL-QAVISKHVQDVSERMASVVDLRI-KRTNEL-LSGVRIVKFM 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches 34; Indels 4; Gaps
                                                                                                                                                          ADDRESSEE: PARTED RESEARCH & DEVELOPMENT INNOVATIONS STREET: Queen's University at Kingston CITY: Kingston STATE: Ontario STATE: Ontario ZIVIRY: CANADA ZIP: K7L 3N6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB 2; Length 1548; Pred. No. 5.85e+01;
                                   Sequence 7, Application US/08460907B
Patent No. 5891724
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUS
TITLE OF INVENTION: RESISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1548 AA; 172282 MW; 12743552 CN;
                                                                                                                                                                                                                                                                                                                  UMBER: US/08/460,907B
05-JUN-1995
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/460,907
CLASSIFICATION: 424
PRIOR APPLICATION DAYA:
APPLICATION DAYA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
FILING DATE: 8-MAR-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERENCE/DOCKET NUMBER: 01551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION POR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGRAT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
                                                                                                                                                                                                                                 ZIP: N.L. J.W.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OBFRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 424
           Sequence 7, Application US/08460907B
                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 2.7%;
Best Local Similarity 28.2%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 GWEPVFLARIQDARSREL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LWKPHYLDPDEGIRFRGL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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g
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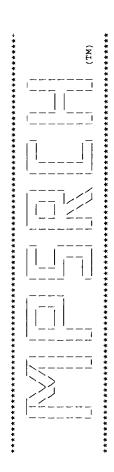
RESULT

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204 KAAQRWVLSNVVERLPVHGAAHGFVAGRSILTNALAHQGADVVVKVDLKDFFPSVTWRRV 263
                                                                                                                                                                                                                                                                                                                    16 RAVQOSNVSNSVRWLQVQTSS-GL-DLRSELVQELIPEQQDRLKKIK-SDMKGSIGNITV 72
                                                                                                                                                                                                                                                                                                                                                            264 KGLLRKGGLPEGTSTLLSLLSTEAPRQAVQFRGKLLHVAKGPRALPQGAPTSPGITNAL 322
                                                                                                                                                                                                                                                                        8; Gaps
                                                                                                        APPLICANT: INOUYE, SUNIKO; HSU, MEI-YIN; EAGLE, SUSAN;
INOUYE, MASAYORI
TITLE OF INVENTION: ISOLATED PACTERIAL REVERSE TRANSCRIPTASE
                                                                                                                                                                                                                                            Score 89; DB 4; Length 485; 
Pred. No. 9.04e+01; 
27; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08742753
Patent No. 5861278
GENERAL INFORMATION:
APPLICANT: WONG, Gordon G.
APPLICANT: YAO, Kwok-Ming
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      763 AA
                                                                                                                                         NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/315,316
FILING DATE: 24-FEB-1989
                                                                                                                                                                                                                     525 AA; 57562 MW; 1459426 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08742753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, SEVENE R.
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                            Query Match 2.6%;
Best Local Similarity 26.9%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                       Patent No. 5320958.
                                                                                             5320958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02140
                                                                                                                                                                                                           LENGIH: 485
                                                                                                                                                                                                                                                                                                                                                                                                            JT 15
US-08-742-753-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                           SEQ ID NO:2:
                                               01-JAN-1900
                                                                                               Patent No.
                                                                                                                                                                                                                     SEQUENCE
                         XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                               đ
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9

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CC TENGTH: 763 amino acids
CC TYPE: amino acids
CC TYPE: amino acids
CC STRANDEDNESS: single
CC TOPOLOCY: linear
CC MOLECULE TYPE: CDNA
CC NAME/KEY: CDS
CC LOCATION: 70.12358
CC LOCATION: 70.12358
CC LOCATION: 70.12358
CC LOCATION: 70.12358
CC LOCATION: 70.1358
CC LOCATION: 70.1358
CC LOCATION: 70.12358
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CC LOCATION: 70.12358
CC LOCAT
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US-08-702-718-2.rag



Pelease 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 18.71 Seconds 535.432 Million cell updates/sec Fri Oct 22 16:20:42 1999; Run on:

Tabular output not generated.

>US-08-702-718-2 (1-471) from US08702718.pep Description: Perfect Score:

Sednence:

PAM 150 Gap 11 Scoring table:

170751 segs, 21266608 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part24 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Mean 36.074; Variance 166.895; scale 0.216 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

					COLLINGO		
		æ					
Result		Query					
No.	Score	Match	Match Length DB	DB	ΩI	Description	Pred. No.
   ref   	3466	100.0	471	15	R86383	Potato citrate syntha	0.00e+00
2	3466	100.0	471	14	R82838	Potato citrate syntha	0.00e+00
e	3098	89.4	469	14	R82840	Tobacco citrate synth	1.27e-270
4	2637	76.1	437	14	R82839	Sugar beet citrate sy	8.02e-228
5	310	8.9	436	m	R14357	Citrate synthase enco	1.16e-15
9	130	3.8	754	35	W69756	Acetobacter xylinum b	2.91e-01
7	113	3.3	220	σ	R47340	Fragment of chromaffi	4.63e+00
80	115	3,3	754	ω	R45000	Cellulose synthase op	3.37e+00
6	110	3.2	3084	35	W50891	Mouse laminin A chain	7.44e+00
10	105	3.0	355	24	W29179	Rat CC chemokine rece	1.63e+01
11	100	2.9		29	W55574	H. pylori ORF 06ep302	3.50e+01
12	100	9.5	329	62	W55330	H. pylori ORF hp3e110	3.50e+01
13	101	2.9	456	34	W38570	Methyl tetrahydropter	3.01e+01
14	100	2.9	4473	13	R97244	Virulence gene cluste	3.50e+01
15	46	2.8	355	25	W26588	Human MIP-1 alpha/RAN	5.51e+01
16	97	2.8	355	11	R52749	C-C chemokine recepto	5.51e+01

0 0

5510 4400 4400 4400 4400 4400 4400 4400	. 346+0 . 346+0 . 346+0 . 866+0 . 406+0 . 076+0 . 076+0 . 076+0
an MIP-lalpha/RA staglandin-EB3-9 staglandin-EB3-2 staglandin-EB3-2 staglandin-EB3-8 an prostaglandin an EB3-V recepto eptococcus pneum se novel secrete shumania antigen ymphocyte TLiSA an T-lymphocyte X accessory mole ceptoia insertio	Human homologue of ye Human RAD50.  NANBY Hutch 629 isola Streptococcus pneumon M. vaccae potb homolo Mouse GRP protein seq P. membranaefaciens W. CF-5 pathogen resista CF-5 pathogen resista CF-5 pathogen resista Human protein compris
W25751 R69518 R69517 R89517 R89516 R870156 R870156 R870186 R870186 R870186 R870186 R870186 R870186 R870186 R870186 R870186 R870186 R870186 R870186 R870186	1234 131 131 131 131 131 131
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	388 383 388 388 388 388 388 388
88888888888888888888888888888888888888	1312 1312 1312 3011 393 393 479 968 1016
$\alpha$	
\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	\$\$\$\$\$\$\$\document{\pi}\$
1111222222222 786012842322321286	

### ALIGNMENTS

Inhibiting citrate synthase (CS) activity in plants - to inhibit flower formation and improve storage capacity, e.g. in potatoes, a lso new CS sense and anti-sense DNA sequences claim 5; Page 15-19; 35pp; German.

Claim 5; Page 15-19; 35pp; German.

C claim 5; Page 15-19; 35pp; German.

C claim 5; Page 15-19; 35pp; German.

C cross of the potato citrate synthase (CS) gene or cDNA sequence encoding CS cross of the plants. Antisense CS sequences are useful for altering CS activity in plants. Antisense CS sequences can be used to inhibit CS expression in plants and has the plant's storage capacity. This is partic, useful in crop plants cof any kind but esp. useful in potatoes. In addition to altering CS activity the DNA sequences can also be used to identify similar sequences in the genomes of other plants and in the production of transgenic plants with altered CS activity. This sequence represents the amino acid sequence of potato citrate synthase. R86383, 24-APR-1996 (first entry) Potato citrate synthase, Citrate synthase; inhibitor; increased storage capacity; potato; (AGRE ) HOECHST-SCHERING AGREVO GMBH. La Cognata U, Landschutze V, Muller-Roeber B, Landschuetze V; WPI: 95-321536/42. N-PSDB; T03410. T 1 R86383 standard; Protein; 471 AA Solanum tuberosum. 14-SEP-1995. 09-MAR-1994; 408629. 09-MAR-1994; DE-408629. 22-SEP-1994; DE-433366. 19-OCT-1994; DE-438821. antisense DNA. RESULT 

Gaps .. Score 3466; DB 15; Length 471, Pred. No. 0.00e+00; 0; Mismatches 0; Indels 0 Query Match 100.0%; Best Local Similarity 100.0%; Matches 471; Conservative

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1 mvfyrsvsllsklrsravggsnvsnsvrwlqvqtssgldlrselvqelipegqdrlkkik 60

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                                                                                     61 SDMKGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGGE 120
                                                                                                                                                                                                                                181 malgvgsefgkayekgihkskyweptyedsmnliagvplvaayvyrrmykngdtipkdes 240
                                                                                                                                                                                                                                                                                                                                     361 tvprytcgrefamkhlpedplfqlvsklyevfllflqnlaklkpwpnvdahsgvllnyyg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 sdmkgsignitvdmvlggmrgmtgllwkphyldpdegirfrglsipecqkvlpaakpgge 120
                                                                                                                                              121 pipegllwllltgkvpskeqvnsivsgiaesgiisliimyttidalpvtahpmtgfatgv 180
                                                                                                                                                                                      121 PLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGV 180
                                                                                                                                                                                                                                                                          181 MALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDES 240
                                                                                                                                                                                                                                                                                                                 241 ldyganfahmlgfsssemhellmrlyvtihsdheggnvsahtghlvasalsdpylsfaaa 300
                                                                                                                                                                                                                                                                                                                                                                                                   Inglagplhglangevllwiksvveecgeniskeglkdyvwktlnsgkvvpgfghgvlrk 360
                                                                                                                                                                                                                                                                                                                                                                                                                                          301 LNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 sdmkgsignitvdmvlggmrgmtgllwkphyldpdegirfrglsipecqkvlpaakpgge 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA fragment of citrate synthase from Arabidopsis thallana was firstly amplified using A.thaliana cDNA and oligos 704202 and 704203 which are complementary to the 5. or 3. end of the coding region of A. thaliana cDNA for citrate synthase. The oligos additionally introduce Bammil cleavage sites at both ends of the amplified cDNA fragment, a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVFYRSVSLLSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIK 60
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Disclosure, Page 53-56; 87pp; English.
To identify a cDNA from potato which codes for citrate synthase, a
                   1 MVFYPSVSLLSKLPSPAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIK
Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ltearyytvlfgvsralgicsqliwdralglplerpksvtmewlengckka 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purified and sequenced. The nt sequence is given in TO4199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Citrate synthase; flower formation; tuber storage. Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3466; DB 14;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Landschutze V, Muller-rober B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R82838 standard; Protein; 471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potato citrate synthase.
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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07-MAR-1995; E00859.
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DNA encoding plant citrate synthase - used to regulate flower formation, to improve strorage of tubers, etc. and to reduce sprouting Disclosure; Page 60-63; 87pp: English
To identify a cDNA from tobacco which codes for citrate
                                                                                                                                                                                                                                                                                                                                                                                                       181 malqvqsefqkayekgihkskyweptyedsmnliaqvplvaayvyrrmykngdtipkdes 240
                                                                                                                                                                                                                                                                                                    Inglagplhglangevllwiksvveecgeniskeglkdyvwktlnsgkvvpgfghgvlrk 360
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                                                                                                PLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGV 180
                                                                                                                                                                                                                      241 ldyganfahmlgfsssemhellmrlyvtihsdheggnvsahtghlvasalsdpylsfaaa 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                 (AGRE ) HOECHST-SCHERING AGREVO GMBH.
La Cognata U, Landschutze V, Muller-rober B, Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radicactive DN probe which comprises Solanum tuberosum citrate synthase CDNA (T04199). One of the clones was sequenced. The nt. sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3098; DB 14; Length 469;
Pred. No. 1.27e-270;
23; Mismatches 22; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 ltearyytvlfgvsralgicsgliwdralglplerpksvtmewlengckka 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobacco citrate synthase.
Citrate synthase; flower formation.
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R82840 standard; Protein; 469
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Local Similarity 89.6%;
es 423; Conservative
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19-OCT-1994; DE-438821
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W69756 standard; Protein; 754
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                                                                                                                                                                 453 LERPKSVTMEWLENGCKK 470
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Best Local Similarity 30.5%;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          (NAKA-) NAKANO SUMISE KK.
WPI; 91-329112/45.
                                                                                                                                                                                                                                                                                                                     27-SEP-1991.
05-FEB-1990; 024395.
15-FEB-1989; JP-033776.
05-FEB-1990; JP-024395.
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               vmalqvqsefqkayekgihksklweptyedsmsliaqvplvaayvyrrmykngntipkdd 238
                                                     239 sldyganfahmlgfsssdmhel-mklyvtihsdheggnvsahtghlvasalsdpylsfaa 297
                                                                                                          298 alnglagplhglangevllwiksvveecgeniskeglkdyawktlksgkvvpgfghgvlr 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 57-60; 87pp; English.

Disclosure; Page 57-60; 87pp; English.

Synthase, a cDNA from sugar beet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepd. Plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solanum tuberosum citrate synthase cDNA (T04199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is given in T04200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 SSGLDLRSELVQELIPEQQDRLKKIKSDMKG-SIGNIIVDMVLGGMRGMTGLLWKPHYLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     La Cognata U, Landschutze V, Muller-rober B, Landschuetze V;
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Pred. No. 8.02e-228;
41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                             Sugar beet citrate synthase.
Citrate synthase; flower formation.
Beta vulgaris strain Zuchtlinie 5S 0026
W09524487.A.
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09-WAR-1994; DE-408629.
22-SEP-1994; DE-438546.
19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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R82839 standard; Protein; 437
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Best Local Similarity 81.3%;
Matches 356; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T04200
                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Gaps 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nyaenflsmmfarmsepykvnpvlaramnrililhadheq-naststvrlagstganpfa 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 DYGANFAHML-G-FSSS-EMHELLMR-LY-VII-HSDHEGGNVSAHTGHLVASALSDPYL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 ciaagiaalwgpahgganeavlk-mlarigk-kenip-afiaq-v-kdknsgvklmgfgh 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 rvyknfdprakimgqtchevltelgikddplldlavel-ekialsddyfvqrklypnvdf 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 GVLRKIVPRYIC-QRE-FA-MKHLP--EDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDA 410
                                                             124 EGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 sa-f-ypdandiaip-an-rdla---amrliakiptiaawayk--ytggeafiyprnd-l 199
                                                                                                                                                                                                                                                                         394 LFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP 452
274 EGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 SFAAALNGLAGPLHGLANQEVLLWIKSVVECGENISKEQLKDYVWKTLNSGKVVPGFGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The aarA gene encodes the citrate synthase and is part of an acetic acid resistance operon comprising aarA, aarB and aarC. The DNA can be used to prepare an acetic acid resistant strain bacteria for use in acetic acid fermentation. See also R14358 and 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; Mismatches 111; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acetic acid resistant gene with in plasmid and transformed acetobacter - improves yield of acetic acid fermentation. Disclosure, Fig 5; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 310; DB 3; Length 436; Pred. No. 1.16e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 ysgiilkamgiptsmf-tvlfavarttg 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 HSGVLLNYYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .T
R14357 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-1992 (first entry)
Citrate synthase encoded by aarA.
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Sun Oct 24 10:10:30 1999

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Claim 2; Page 34; 50pp; Japanese.

This represents the amino acid sequence of a Acetobacter xylinum subspecies sucrefermentans bcsA gene product. The invention provides a gene encoding a Acetobacter xylinum subspecies sucrefermentans derived cellulose synthesis complex produced protein. The gene sequence represents bcsA, bcsB, bcsC or bcsD, CMCase and a beta-glucosidase encoding gene. The novel gene and the enzyme participate in the synthesis of cellulose by microorganisms. Cells transformed with the genes may be sequence 754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ώ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 plaflfaggniiaaaplavaayalphmfhsiata-akv-nkg-wrysfwsevyettmalf 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 SLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 lvrvtivtllfpskgkfnvtekggvlxeexfdlgatypnii-fatimmgglliglfeliv 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 IAQVPLVAA-YVYRRMYKNGDT--IPKDESLDYGANFAHMLGFSSSEMHELLMRLYYTIH 270
                 Acetobacter xylinum; sucrófermentans; cellulose synthesis complex; bcsA; bcsB; bcsC; bcsD; CMCase; beta-glucosidase; enzyme; cellulose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Gaps
Acetobacter xylinum bcsA gene product.
Acetobacter xylinum; sucrofermentans; cellulose synthesis complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene encoding Acetobacter xylinum cellulose synthetase complex - containing a group of genes including those for conventional and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mammalian vesicle membrane transport protein - and corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vesicle membrane transport protein; gene therapy; screening; Parkinsons disease; neurotoxin; identification; detection; antibody; probe; chromaffin granule amine transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 130; DB 35; Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragment of chromaffin granule amine transporter protein.
                                                                                                                                                                                                                                                                                                                                              (BIOP-) BIO-POLYMER RES CO LTD.
Hayashi T, Tahara N, Tonouchi N, Tsuchida T, Yano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.91e-01;
                                                                                                                                                                                                                                     /label= unspecified
/note= "encoded by AAG"
                                                                                                                                            'note= "encoded by GAG"
                                                                                                                                                                                                 /note= "encoded by GAG"
                                                                                                                             /label- unspecified
                                                                                                                                                                                /label= unspecified
                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 SDHEGGNVSAHTGHLVASA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.8%;
Best Local Similarity 19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1992; US-899074,
30-JUL-1992; US-923096,
(REGC ) UNIV CALIFORNIA,
Edwards RH;
                                                                                                                                                                                                                                                                                                                             JP-063927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1993; U05704.
                                                                      Acetobacter xylinum.
                                                                                                                                                                                                                                                                                         11-SEP-1998.
09-OCT-1997; J03633.
04-MAR-1997; JP-0639
                                                                                                          Misc_difference 503
                                                                                                                                                               Misc_difference 506
                                                                                                                                                                                                                    Misc_difference 573
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 98-495854/42.
N-PSDB; V52831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus rattus.
                                                        microordanism
                                                                                                                                                                                                                                                                         409839455-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                      Yoshinaga F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9325699-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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four genes, genes A-D. The operon sequence may be used in a transcription vector for the expression of the cellulose synthase operon to increase cellulose production in a recombinant microorganism. This system may be used as an important tool for exploring mechanisms of cellulose synthesis and for enhancing production of cellulose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 SLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 plaflffggnijaasplavlayaiphmfhsiata-akv-nkg-wrysfwsevyettmalf 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 DSMNLIAQVPLVAAYVYRRMYKNGDT-IPKDESLDYGANFAHM-LGFSSSEMHELLMRLY 266
                                                                                                                                                                                                                                                             of neurotoxins or psychiatric disorders and to identify compounds which selectively inhibit or activate its action. Antibodies raised against this protein are useful as immunoassay reagents for detecting the protein and as affinity reagents for purification. This fragment of the transporter protein shares homology with the N-terminal domains of the methlenomycin; tetracycline and multi-drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 dnmlltvvvpivptflyatefkdsnsslhrgpsvssqeenvrigilfaskalmqllvnpf 83
DNA, vectors, transformed cells and antibodies, for diagnosis and treatment of neurological disorders. e.g. Parkinson disease Example 2: Page 114-115; 181pp; English.

The CDNA encoding the chromaffin granule amine transporter protein is useful in gene therapy and as a probe for detecting genomic sequences. The protein is used for screening cytotoxic compounds implicated in Parkinsons disease, diseases associated with activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 50; Fig 1; 79pp; English.

The sequences given in R45000-03 represent the proteins encoded by the bacterial cellulose synthase operon. The sequence given in R45004 is the begining of an open reading frame overlapping the end of this operon. The bacterial cellulose synthase operon contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contiguous nucleic acid sequences - encoding bacterial cellulose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose synthase operon, gene A product.

Bacterial; cellulose synthase; operon; gene A; gene B; gene C; gene D; transcription vector; recombinant microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calhoon RD, Fear AL, Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.3%; Score 113; DB 9; Length 220; Best Local Similarity 20.2%; Pred. No. 4.63e+00; Matches 22; Conservative 41; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 VIIHSDHEGGNVSAHIGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 vgpltnrigyhipmfvgfmimf-lstlmfafsgtyallfvartlggigs 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             л 8
R45000 standard; Protein; 754 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transporter proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 18.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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R, Wong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1993.
12-APR-1989; 337194.
04-APR-1990; WC-U01811.
09-APR-1990; IL-094053.
10-APR-1990: CA-014264.
11-APR-1990; NZ-233312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellulose synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetobacter xylinum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 93-404004/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Q53522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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3084 AA;

Sequence

SO

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214 IAQVPLVA-AYVYRRMYKNGDT--IPKDESLDYGANFAHMLGFSSSEMHELLMRLY-VTI 269
477 lvrvtiitlmfpskgkfnvtekggvleeeefdlgatypnii-fagimtlglliglfeltf 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the mouse laminin A chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin Broducts (see W50888-98) may include mouse or human laminin A or Al Chain, laminin Bl or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the qlobular repeats of the laminin A1 chain and the beta-amyloid binding domain of the laminin A chain, an employed disease comprises administering a method for treating an amyloid disease comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldit-Jacob diseases, Gerstmann-Straussler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin).
                                                                                                                                                                                                                                                                                                                   Wouse laminin A chain.

Wouse laminin A chain.

Wouse laminin A chain.

Wouse laminin mouse; beta amyloid; amyloidosis; Alzheimer's disease;

Down's syndrome; hereditary cerebral heamorthage; inflammation;

malignancy; Familial Mediterranean Fever; multiple myeloma;

Galest, Faminial Mediterranean Fever; multiple myeloma;

Gertstmann-Straussler syndrome; kuru; scrapie; haemodialysis;

carpal tunnel syndrome; senile cardiac amyloid polyneuropathy;

Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide having a conformational similarity to a fragment of a mannin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation-association amyloidosis), the amyloidosis associated with multiple myeloma and other B-cell abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
2746..2922
/note= "fourth globular domain repeat (Claim 13)"
2690..2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wrl; y=240334/21.
Use of laminin and fragments - for developing products for use in
the diagnosis and treatment of amyloid disease, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "beta-amyloid protein binding region (Claim 12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 74-79; 132pp; English.
                                                                                                                                                                                                                                                 W50891 standard; Protein; 3084 AA.
                                                                                                                                                                                                                                                                                                 07-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1998.
08-OCT-1997; U18145.
08-OCT-1996; US-027981.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snow AD;
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                                                                                              536 hfnqlag 542
                                                                                                                                                270 HSDHEGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease or CJD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09815179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castillo G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy
                                                                                                                                                                                                                                                                              W50891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
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This sequence is a rat CC chemokine receptor. The receptor can be used
to screen for novel binding compounds and for preparation of antibodies
                                                     1884 selqsragaldrdlenvrwvslnatsaahvhsn-iqtlt-eeaewla-adahktanktdl 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 lfnlavsdlvflftlpfwidy-klkdnwvfgdamckllsgfyylglyseiffiilltidr 131
                                                                              11 SKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIGNI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105; DB 24; Length 355;
Pred. No. 1.63e+01;
15; Mismatches 38; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC chemokine receptor protein - useful to screen for novel binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori
  Length 3084;
                          Indels
                                                                                                                                                                                                              19-DEC-1997 (first entry)
Rat CC chemokine receptor.
rat; CC chemokine receptor; screen; binding; ligand.
 Score 110; DB 35; L
Pred. No. 7.44e+00;
30; Mismatches 33;
                                                                                                         1941 ise-slas-rgkavlqrssrflkesvgtr 1967
                                                                                                                                   71 TVDMVLGGMRGMTGLLWKPHYLDPDEGIR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 ylaivhavfslrartvtfgiitsiii-w 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 ALGICSQLIWDRALGLPLERPKSVTMEW 463
                                                                                                                                                                          T 10
W29179 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 11
W55574 standard; Protein; 329 AA.
                                                                                                                                                                                                                                                                               02-SEP-1997.
22-FEB-1996; 035192.
22-FEB-1996; JP-035192.
(TAKE) TAKEDA CHEM IND LTD.
WPI: 97-486426/45.
N-PSDB; T86839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 31.8%; les 28; Conservet:
7. Match 3.2%;
Local Similarity 23.6%;
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-1996; US-758731.
25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
(ASTR ) ASTRA AB.
Alm RA, Smith D:
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1997; U05223
                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AA;
                                                                                                                                                                                                                                                         rattus.
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J09227599-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 antiserum
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                                                                                                                                                                                                                                                                                                                                                                                compounds
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 Query Match
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infection and for diagnosis of H. pylori infection

Claims 14.96; Page 779-779; 1145pp; English.

This sequence is a H. pylori cytoplasmic protein involved in cofactor

metabolism. The protein may be used in a vaccine to prevent or treat H.

pylori infection or to identify H. pylori polypeptide binding compounds,

useful as potential H. pylori life cycle activators or inhibitors. The

DNA and probes derived from it may be used for the identification of

H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic

acid sequences complementary to the DNA act as antisense sequences and

can be used to prevent the translation of H. pylori infection. Nucleic

and distribution of H. pyloris pecific antigens. The genomic sequence of

H. pylori (ATC 55679) was determined from overlapping contigs generated

by mechanically shearing the bacterial DNA. The sequences were analysed

for ORP of at least 180 nucleotides, and the predicted coding regions

cefined by computer evaluation. To identify likely H. pylori antigens for

vaccine development, the amino acid sequences predicted from various ORF

were analysed for significant homology to other known or exported

membrane proteins. Having identified and determined the sequences of

interest, particular regions can be isolated from H. Pylori by 2CR

amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.

This sequence is a H. pylori protein of unspecified function.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori plypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic and sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATC. 55479) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for OR of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-1998 (first entry)
H. pylori ORF hp3el1024orf49 protein.
H. pylori oRF hp3el1024orf49 protein.
Yctpplasmic, vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 100, DB 29; Length 329;
Pred. No. 3.50e+01;
15; Mismatches 8; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 IAOVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 veempliasvifnrl-kkgmplqmdgalny-qefsh 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r 12
W55330 standard; Protein; 329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.9%,
Best Local Similarity 30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1997; UO5223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASTR ) ASTRA AB.
Alm RA, Smith D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; V24739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W55330;
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Claim 12; Pages 342-344; 483pp; English.

This sequence represents a Streptococcus pneumoniae protein that, based on homology with an E. coli protein, is a methyl tetrahydropteroyitri glutamate-homocysteine methyltransferase, and is encoded by a DNA of the invention. The DNA sequences were isolated from S. pneumoniae strain 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antaqonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or I cell immune responses to protect the animal from disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            profeins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenessis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 vyadlvnlpvdaigl-dfvegkktlelvkggfpadktlyvgivngkniwrnnyekslavl 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methyl tetrahydropteroyltriglutamate-homocysteine methyltransferase. Streptococcus pneumoniae protein; genetic immunisation; antiquonist; immunological response; inoculation; antibody production; inhibitor. I cell immune response; antimicrobial compound; bacterial adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 34; Length 456;
Pred. No. 3.01e+01;
17; Mismatches 22; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       extracellular matrix protein; protein mediated cell invasion, wound;
                                                                                                                                                                                                         8; Indels 2; Gaps
                                                                                                                                                           Score 100; DR 29; Length 329;
Pred. No. 3.50e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black MI, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                       218 veempliasvifnrl-kkgmplqmdgalny-qefsh 251
                                                                                                                                                                                                                                                                                                  214 IAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAH 249
                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            W38570 standard; Protein; 456 AA.
W38570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-1997; U07950.
14-MAY-1996; US-017670.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%;
Local Similarity 31.3%;
Les 20; Conservative
                                                                                                                                                           Query Match 2.9%;
Best Local Similarity 30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-1998 (first entry)
                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 98-008793/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 AA;
                                                                                                                 329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections
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                                                                                                                    Seguence
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                                                                                            hosts.
                                                                                                                                                                                                         Matches
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Tribuly insuration inactivated genes into environment and retrieval and analysis of mutants

Tribuly insuration inactivated genes into environment and retrieval and analysis of mutants

Tribuly insurably for microorganism having a reduced adaptation

Claim 51: Figure 11: 131pp; English.

A method for identifying a microorganism having a reduced adaptation

Claim 51: Figure 11: 131pp; English.

A method for identifying a microorganism having a reduced adaptation

Comprision to a particular environment comprising the insertional inactivation of a gene with a nucleic acid comprising

Tribulative of microorganisms each of a gene with a nucleic acid comprising

Tribulative of microorganisms of the said microorganism; (2) providing

Tribulative sequence for any stored any each mutant produced by step (1) and

Troviding individually stored enceleic acid comprising the unique marker sequence from each individual mutant; (3) introducing a

Troviding individually stored microorganisms which are able to do so

Compress in the said environment; (4) into the said particular environment and allowing those microorganisms; (5) comparing any

Compress in the nucleic acid isolated in step (4) to the marker sequence of each individual mutant which does not contain any

Compress the marker sequence of each individual mutant which does not contain any contain mathor can be used for identify with individual mutant with does not contain and contain mathor can be contain with the marker sequences in the microorganisms of the marker sequences of each individual mutant which does not contain any contain mathor can be contain with the marker sequences in the microorganisms of the marker sequences as isolated in step (4). The products as in step contain mathor and be contained to the marker sequences in the microorganisms of the marker sequences in the micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100; DB 19; Length 4473;
Pred. No. 3.50e+01;
25; Mismatches 35; Indels 4; Gaps 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2872 mrtixxrsrscherysms-lpdspl-qligilfllsilpl-ilvmgtsflklavvfsilr 2928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the marker sequences as isolated in step (4). The products and methods can be used for identifying virulence genes in microorganisms. The mutant microorganisms can be used in vaccines or to screen for drugs which reduce virulence or compounds useful for preventing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-1998 (first entry)
Human MIP-1 appha/RANTES receptor.
Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
reduced upon activation normal T expressed and secreted; RANTES;
                                                                         07-13N-1997 (first entry)
Virulence gene cluster polypeptide product.
Virulence gene cluster polypeptide product.
Whitant, adaptation, virulence factor; identification; screening;
Vaccine; drugs; infection: treatment.
Salmonella typhimurium.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Noyer= "All x's in this sequence correspond to termination codons in the virulence gene cluster sequence given in T09224."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ameliorating or treating infections in animals or plants. Sequence 4473 AA;
R97244 standard; Protein; 4473 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2929 nalgiqqvppnialyglalvlsl 2951
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W26588 standard; Protein; 355 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-1996.
11-DEC-1995; GQ2875.
09-DEC-1994; GB-024921.
31-JAN-1995; GB-001881.
05-MA-1995; GB-009239.
(RPMS-) RPMS TECHNOLOGY LTD.
Holden DW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.9%;
Best Local Similarity 22.9%;
Matches 19; Conservative
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N-PSDB; T09224.
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                                                  NAME OF THE PROPERTY OF THE PR
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Www receptor; cytokine; antiinflammatory; inflammation; human.

S Homo sapiens.

WE5652133-A.

PD 29-JUL-1997.

29-JUL-1997.

29-JUL-1993; 012988.

R 28-JAN-1993; 012988.

PI Murphy PM;

PT 392945/36.

M NPDB; 190384.

PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop products for the detection of these cytokine(s) and their receptors.

PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop products for the detection of these cytokine(s) and their receptors.

PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop products for the detection of these cytokine(s) and their receptors.

PT MIP-1-alpha and RANTES receptor for human macrophage conflammatory protein-1 alpha (MIP-1 alpha) and regulated upon acidiammatory protein-1 alpha (MIP-1 alpha) and regulated upon acidiammatory protein-1 alpha (MIP-1 alpha) and regulated upon acidiammatory protein-1 alpha/RANTES receptor concleotides; a cell transformed or transfected with the nucleic concleotides; a cell transformed or transfected with the nucleic concleotides; a cell transformed or transfected with the nucleic concleotides; a cell transformed or transfected with the nucleic concleotides; a cell transformed or transfected with the nucleic concleotides; a cell transformed or transfected with the nucleic concleotides; a cell transformed or transfected with the nucleic concleotides; a cell transformed or assay for MIP-1a/RANTES in creeptor and polymorphisms in physiological samples. In addition, the coeptor can be expressed and used to assay for MIP-1a/RANTES in creeptor concleotides and prospective usefulness of new antiinflammatory agents.

Sequence 355 AA;

Sequence 355 AA;
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Query Match 2.8%; Score 97; DB 25; Length 355;
Best Local Similarity 31.9%; Pred. No. 5.51e+01;
Matches 23; Conservative 14; Mismatches 29; Indels 6; Gaps

Ob 65 lknmtsiyllnlaisdllfftlpfwidy-klkddwvfgdamckilsgfyytglyseiff 123

9

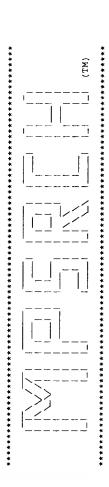
Db 124 iilltidrylai 135

QY 428 TVLFGVSRALGI 439

Search completed: Fri Oct 22 16:28:26 1999 Job time : 464 secs.

		:

US-08-702-718-2.rpr



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:28:44 1999; MasPar time 21.02 Seconds 897.635 Million cell updates/sec Pun on:

Tabular output not generated

>US-08-702-718-2 (1-471) from US08702718.pep 3466 1 MVFYRSVSLLSKLPSPRAVQQ........PLERPKSVTMEWLENGCKKA 471 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 50.591; Variance 106.019; scale 0.477 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

SUMMARIES	Description Pred. No.	44316 ethanolamine ammonia 0.00e+00	probable citrate (si)	citrate (si)-synthase 0.	citrate (si)-synthase 0.	0 citrate (si)-synthase 0.	citrate (si)-	citrate (si)-	citrate (si)-synthase 4.	14-nm filament protei 8.	citrate (si)-synthase 9.	citrate (s1)-synthase 3.00e-	citrate	citrate (si)-synthase 1.	citrate s	citrate synthase gltA 4.	citrate synthase (cit 9.	:39506 citrate (si)-synthase 1.41e-22	citrate	citrate	probable dltA2 protei 4.	citrate (si)-synthase 4.	citrate synthase III 1.	
SUMMARIES	DB ID	1 2 \$44316	4 2 T02390	1 YKMUM	1 YKPG	2 \$42370	1 YKBY	2 S41563	1 YKBYC	2 JC5625 I	2 S52814 C	2 I40717	1 YKOPC	1 YKPSCA	2 S53007	2 S74344	2 C69417	2 I39506	2 JQ1392	2 A43936	1 2 E70782	6 1 YKRECP	2 2 E69658	110011
æ	Query Match Length	100.0 47	81.4 47	۲.		49.7 468	_	~	_	8.3	33.7 486		σ.	∞.		7.6 39				7.2 37	43	43	37	
	Score	3466	2820	2305	1921	1722	1663	1606	1575	1329	1168	316	307	272	566	263	261	254	254	249	251	245	242	000
	Result No.		CI	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	,

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301 LNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRK 360

361 TVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYYG 420

citrate (si)-synthase 1.37e-18 429 2 \$41527 citrate (si)-synthase 1.34e-17 citrate (si)-synthase 1.34e-17 citrate (si)-synthase 1.34e-17 citrate synthase 1.16e-15 389 2 E64760 citrate synthase 1 (c 2.01e-11 386 2 140380 citrate synthase 1 (c 2.01e-11 385 1 YKYT citrate (si)-synthase 1 (c 2.01e-11 426 2 E64523 citrate synthase - He 2.36e-10 375 1 YKMY citrate (si)-synthase 2.18e-07 YKMY citrate (si)-synthase 1.14e-07 YKMY probable citrate synthase 1.36e-03 754 2 E70781 probable citrate synthase 2.18e-07 470 2 S78686 hypothetical protein 5.41e-01 470 2 E70384 blotin synthetese A 1.59e-00 1 474 2 A42383 mycblast citry protein 5.41e-01 470 2 H9339 mycblast citry protein 9.32e-01 1970 2 T00284 mycblast citry protein 9.44 2 S76188 alpha-sl-casein precu 4.54e+00 8.46e-00 4.65e-00 4.6	ALIGNMENTS  S44316  #type complete ethanolamine ammonia-lyase (EC 4.3.1.7) - potato #formal_name Solanum tuberosum #common_name potato 08-Sep-1994  #sequence_revision 10-Nov-1995  #text_change 08-Sep-1997 S44316 Landschuetze, V.: Willmitzer, L.: Mueller-Roeber, B. submitted to the EMBL Data Library, September 1993 S44316 e_type mRNA s	100.0%; Score 3466; DB 2; Length 471; arity 100.0%; Pred. No. 0.00e+00; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	MVFYRSVSLLSKLRSRAVQQSNVSNSVRMLQVQTSSGLDLRSELVQELIPEQODRLKKIK 60 	SDWKGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKFGGE 120 	EGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPV"AHPMTQFATGV 180 	WALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRYYKNGDTIPKDES 240 
&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&&	S4431 ethan #form 08-e 08-e 08-e 34431 S4431 SA4	it ns	SVSLLSK	SIGNITA	EGLLWLLLTGKV            EGLLWLLTGKV	SSEFOKA             SSEFOKA
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45000000000000000000000000000000000000	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #submission #accession	Query Best L Matche	ag oy	0 do 6	Db 12 Qy 12	Db 18 Qy 18

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carbon-carbon lyase; oxo-acid-lyase; tricarboxylic acid cycle
#length 474 #molecular-weight 52782 #checksum 6960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana chromosome II BAC F411 genomic sequence 102390
T02390 *type complete probable citrate (si)-synthase (EC 4.1.3.7) - Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 KSDM-KGSIGNITVDMVLGGMRGMIGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AEPLPEGLLWLLLTGKVPSKEQVEALSKDLANRAAVPDYV-YNAIDALPSTAHPMTQFAS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 GVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARVPVVAAYVYRRMYKNGDSIPSD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 ESLDYGANFAHMLGFSSSEMHELLMRLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 RNTDPRYVCQREFALKHLPDDPLFQLVSKLYEVVPPVLTELGKVKNPWPNVDAHSGVLLN 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17/3; 39/3; 53/3; 75/3; 97/3; 135/3; 157/1; 184/3; 201/2; 227/2, 270/2; 284/3; 313/3; 347/3; 383/3; 400/3; 425/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 KSLDYGANFSHMLGFDDEKVKEL-MRLYITIHSDHEGGNVSAHTGHLVGSALSDPYLSFA 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
                                                                                                                                                                                                                                                                                                                                      #formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKSQL-QELIPEQQDRLKKL 59
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                                                                                                                                                                                                                                                                                                                                                                                       05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 HYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLALERPKSVTMDWLEAHCKKA 471
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9
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                                                                           421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                   421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENOCKKA 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.00e+00;
55; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.4%; Score 2820; DB 2; Best Local Similarity 79.1%; Pred. No. 0.00e+00; Matches 375; Conservative 55; Mismatches 38
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                                                                                                                                                                                                                                                                                      thaliana
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#introns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSIONS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARY
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##cross-references EMBL:X17528; NID:g11243; PID:e1188578; FID:g2652924
##note the Sequence from Fig. 2 is inconsistent with that from
the Sequence from Fig. 2 is inconsistent with that from
Fig. 1 in having 47-Gly, 125-Trp, 141-Leu, 151-Ser,
185-Asn, 187-Asn, 191-Asn, 348-Leu, an additional Gly
after 89-Trp, an additional Val after 393-Cys and two
additional Arg after 228-Arg, in lacking 114-Leu and
residues 233 to 241
                                                                                                                          citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                     Unger, E.A.; Hand, J.M.; Cashmore, A.R.; Vasconcelos, A.C. Plant Mol. Biol. (1989) 13:411-418
Isolation of a cDNA encoding mitochondrial citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 KSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GGLNHYRRSFVASLNWKGTL-AKSKLKH-CRKTWNRAAVSDYV-YNAIDALPSTAHPMTQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 SFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYGH 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 SFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGH 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 GVLRNTDPRYVCQREFALKHHPDDPLFQ-CCKLMKL-ASCLTELESEEPWPNVDAHSGVL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 GVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 GG-EPLPEGLL-WLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTO 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKSQL-QELIPEHKDRLKKL 59
                                                                                                                                                                                #formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 PSDKSLDYGANFSHMLGFDDERLKEL-MRLTSPSTVMHEGGNVSAHTGHLVGSALSDPYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #region acetyl-CoA binding *status predicted\
#active_site His, His, Asp *status predicted
#length 472 #molecular-weight 52941 #checksum 9626
418 YYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.5%; Score 2305; DB 1; Length 472; Best Local Similarity 68.9%; Pred. No. 0.00e+00; Matches 328; Conservative 60; Mismatches 76; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *superfamily citrate (si)-synthase carbon-carbon lyase; homodimer; mitochondrion; oxo-acid-lyase; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                            from Arabidopsis thaliana
*cross_references_MUID:91370823
                                                                                                       *type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession JAVLY.
##molecule_type mRNA
##molecule_type mlNA
1-472 ##label UNG
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#### \*authors Evans, C.T.; Owens, D.D.; Sumegi, B.; Kispal, G.; Srere, P.A. #journal Blochemistry (1988) 27:4680-4686 | Isolation nucleotide sequence, and expression of a cDNA encoding plg citrate synthase. pig citrate (si)-synthase (EC 4.1.3.7) precursor - pig #formal\_name Sus scrofa domestica #common\_name domestic 15-Oct-1982 #sequence\_revision 30-Sep-1992 #text\_change Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Wade, R.D.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.; Titani, K. Proc. Natl. Acad. Sci. U.S.A. (1981) 78:5381-5385 Primary structure of porcine heart citrate synthase. Aci347 Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Walsh, K.A.; Biochemistry (1982) 21:2028-2036 Complete amino acid sequence of porcine heart citrate 416 LNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471 #authors Remington, S.; Wiegand, G.; Huber, R. #journal J. Mol. Biol. (1982) 158:111-152 #title Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7 #cross-references WUID:83010291 ##cross-references EMBL:M21197; NID:g164418; PID:g164419 NCE A90457 #type complete ##molecule\_type protein ##residues 28-464 ##label BLO ##molecule\_type protein ##residues 1-464 ##label EVA A29965; A01109; A51347 #cross-references MUID:82231993 #accession A01109 18-Sep-1998 Titani, K. synthase ##molecule\_type mRNA A29966 A61347 A29966 A92884 ##residues #accession #accession \*contents #journal #authors #authors #journal ACCESSIONS #title #title REFERENCE REFERENCE REFERENCE REFERENCE TITLE ORGANISM RESULT ENTRY DATE ò

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##molecule_type DNA
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                                                                                                                                                                                                                                                                                    annotation; X-ray crystallography, 2.7 and 1.7 angstroms Cirate (si)-synthase is found in nearly all cells capable of catadative metabolism. It catalyzes the condensation of oxaloacetate and acetyl-CoA to form citrate in the tricarboxylic
                                                                                                                                                                                                                                                                                                                                                                                                         It is synthesized in the cytoplasm but functions in the mitochondrion of eukaryote cells. This molecule is a dimer of identical chains. Each dimer binds two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecules of acetyl-CoA and two molecules of oxaloacetate at two
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#modified_site N6,N6,N6-trimethyllysine (Lys) #status
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predicted #label SIG\
#product citrate (si)-synthase #status experimental
#label MAT\
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27 SASSTNLK-DILADLIPKEQARIKTFRQQHGNIVVGQITVDMMYGGMRGMKGLVYETSVL 85

301,347,402

28-464

KEYWOPDS FEATURE 1-27

COMMENT

Query Match

SUMMARY

Matches

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S42370 *type complete citrate (si)-synthase (EC 4.1.3.7) precursor - Caenorhabditis
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                                                                                                                                                                                                                                                   153 IISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEFTYEDSMN 212
                                                                                                                                                                                                                                                                                                            205 LIAKLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFINMLGYIDAQFTEL-MRLYLTIHS 263
                                                                                                                                                                                                                                                                                                                                            264 DHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDV 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 SDEKLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 VPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 FLLFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 NARADLPTHVV-RMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYE 202
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                                                                                   86 DPDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKPA 145
                                                                                                                                        93 DPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESG 152
                                                                                                                                                                                                 146 ALPSHVV-TMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 SKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEV 391
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34 ISSGLDLPSELVQELIPEQQDFLKKIKSDMKGSI-GNITVDMVLGGMRGMTGLLWKPHYL 92
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carbon-carbon lyase; mitochondrion; oxo-acid-lyase
#length 468  #molecular-weight 51540  #checksum 2659
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Pred. No. 0.00e+00;
84; Mismatches 109;
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Matches 236; Conservative
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Suissa, M.; Suda, K.; Schatz, G.
EMBO. J. (1984) 3:1773-1781
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                      citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial yeast (Saccharomyces cerevisiae) protein NVO19; protein VNO01c #formal_name Saccharomyces cerevisiae #formal_name Saccharomyces cerevisiae 25.Feb-1985 #sequence_revision 10-Feb-1995 #text_change
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submitted to the EMBL Data Library, January 1994
Twelve open reading frames revealed on the 23.6 kbp segment
flanking the centromere on the Saccharomyces cerevisiae
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##note the nucleotide sequence was submitted to the EMBL Data
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Fast (1994) 10:1355-1361
Twelve open reading frames revealed in the 23.6 kb segment
flanking the centromere on the Saccharomyces cerevisiae
                           268 TIHSDHEGGNVSAHTGHLVASALSDFYLSFAAALNGLAGPLHCLANQEVLLMIKSVVEEC 327
                                                                                                                                                                                             382 LYKITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIW 440
                                                                                                                                                                                                                      262 VIHSDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEI 321
                                                                                               322 GFNYTEEQLKEWVWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVST 381
                                                                                                                                             328 GENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSK 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
##residues 1-479 ##label LIN
##cross-references EMBL:223259; NID:9313749; PID:9313750
ENCE 845118
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NCE S48338
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#accession A01110
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##cross-references BMBL:271616; NID:91302468; PID.e239778; FID:91302469, MIPS:YNR001c
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predicted #label TNP\
#product citrate (si)-synthase #status predicted #label
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oxo-acid-lyase; tricarboxylic acid cycle
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90; Mismatches 106; Indels
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##cross-references SGD:S0005284; MIPS:YNR001c
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*#molecule_type DNA

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1-479 ##label AER
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P.A.; Guarente, L.P.
MOI. Cell. Biol. (1986) 6:4509-4515
Mitochondrial and nonmitochondrial citrate synthases in
Saccharomyces cerevisiae are encoded by distinct homologous
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Ferea, T.; Contreras, E.T.; Oung, T.; Bowman, E.J.; Bowman,
                                   #journal Mol. Gen. Genet (1994) 242-105-110 Characterization of the cit-1 gene from Neurospora crassa encoding the mitochondrial form of citrate synthase. #cross-references MUID:94104594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Saccharomyces cerevisiae)
protein YCR005c; protein YCR043
#formal_name Saccharomyces cerevisiae
30-Sep-1992_#sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKBYC #type complete citrate (si)-synthase (EC 4.1.3.7), peroxisomal - yeast
                                                                                                                                                                                                                                     36/3; 58/2; 123/1; 453/2
superfamily citrate (s1)-synthase
carbon-carbon lyase; mitochondrion; oxo-acid-lyase
#length 469 #molecular-weight 52002 #checksum 490
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                                                                                                                                                                                                                                                                                                                                                     Length 469;
                                                                                                                                                                                             ##cross-references EMBL:M84187; NID:g168774; PID:g168775
                                                                                                                                                                                                                                                                                                                                                   Ouery Match 46.3%; Score 1606; DB 2; Length 46's Best Local Similarity 54.8%; Pred. No. 2.64e-284; Matches 235; Conservative 79; Mismatches 106; Indels
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                                                                                                                  *accession Assss
*#molecule_type DNA
1-460 ##label ROS
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#accession A25393
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#authors Biteau, N.; Fremaux, C.; Hebrard, S.; Menara, A.; Aigle, M.; Crouzet, M.

#journal Yeast (1992) 8:61-70

#title The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae.

#cross_references Mulb:92254505

#accession S26734
                                                                                                                                                                                                                                                                                                                                   ##cross-references EMBL:X59720; NID:g1907116; FID:e264468; PID:q1907148
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CLASSIFICATION #superfamily citrate (si)-synthase
    acetyl-CoA; carbon-carbon lyase; homodimer; oxo-acid-lyase;
    REYWORDS
    peroxisome; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #region peroxisome location signal (S-[RKH]-L) motif/
#active_site His, His, Asp #status predicted
#length 460 #molecular-weight 51413 #checksum 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 GSVWEGSVLDPEDGIRFRGRTIADIQKDLPKAKGSSQPLPEALFWLLLTGEVPTQAQVEN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 IVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 SYTFEDSLDLLGKLPVIAAKIYRNVFKDGKMGEVDPNADYAKNLVNL1GSKDEDFVDL-M 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 RLYLTIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEVLEWLFAL 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 KEEVNDDYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHFPDYELFK 367
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Mol. Cell. Biol. (1991) 11:38-46
Intramitochondrial functions regulate nonmitochondrial
citrate synthase (CIT2) expression in Saccharomyces
cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                Aigle, M.; Biteau, N.; Crouzet, M. submitted to the Protein Sequence Database, March 1992
##cross-references EMBL:Z11113; NID:93297; PID:93299; GB:M14686;
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Local Similarity 50.5%; Pred. No. 4.46e-278;
tes 222; Conservative 93; Mismatches 120;
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                                                                                                                                                                                                                                                         translation not shown
                                                                                                                                                                                                                                                   1-24 ##label LIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
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predicted #label TNP\
#product 14-nm filament protein/citrate synthase #status
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##residues
1-62 ##label NUM
##rcross-references GB:D90117; NID:9217406; PID:d1014848; PID:g1688046
##cross-references GB:D90117; NID:g217406; PID:d1014848; PID:g1688046
##more
part of this sequence, including the amino end of the
mature protein, was confirmed by protein sequencing
This protein is involved in oral morphogenesis preceding binary
fission, and in nuclear events during fertilization, such as
formation of gametic pronuclei and zygote formation of gametic
pronuclei. It also acts as a mitochondrial enzyme, citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Numata, O.; Takemasa, T.; Takagi, I.; Hirono, M.; Hirano,
Chiba, J.; Watanabe, Y.
Biochem Biophys Res. Commun. (1991) 174·1028-1034
83 GIIFRGYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQN 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 NLKK-VIAEIIPQKQAELKEVKEKYGDKVVGQYTVKQVIGGMRGMKGLMSDLSRC-DPYQ 82
                                                                                                                                                                                                                                                                                                               #formal_name Tetrahymena thermophila
14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blochem Riophys Res Commun (1997) 237:205-210
Direct demonstration of the bifunctional property of
Terrahymena 14-nm filament protein/citrate synthase
following expression of the gene in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetrahymena 14-nm filament-forming protein has citrate
                                                                                                                                                                                                                                        14-nm filament protein/citrate synthase (EC 4.1.3.-)
    Tetrahymena thermophila (SGC5)
49K filament-forming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 462 #molecular-weight 52575 #checksum 9423
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oxo-acid-lyase
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46.8%; Pred. No. 8.43e-229;
vative 95; Mismatches 124;
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*cross-references MUID:91128358
                                                                      428 LITDRAIGASIERPKSYSTE 447
                                                                                                                    443 LIWDRALGLPLERPKSVTME 462
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Conservative
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nes 207; Conser
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Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, T.D.; Hall, J.; Storms, R.K.; Vo, D.H.; Winnett, E. submitted to the EMBL Data Library, July 1995

The sequence of Saccharomyces cerevisiae chromosome XVI right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references EMBL:U31900; NID:q1276597; PID:q939735; MIPS:YPR001w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross.references EMBL:248951; NID:9762999; PID:9763000; MIPS:YPR001w##experimental_source strain AB972
NO.E. S57724
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                                                                                                 321 KVSDKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCA 380
                                                                                                                                                                                                                                                                     381 DVIPKKLLTYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSR 439
                                                                                                                                                                                                                                                                                               80 SLDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELA 139
                                                                                                                                                                                                                    330 NISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLY 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        citrate (si)-synthase (EC 4.1.3.7) - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 IIKSSALTLKEAL-ENVIPKKPDAVKKLKACYGSTFVGPITISSVLGGMPGNQSMFWQGT 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein LPZ1w; protein YP9723.01; protein YPR001w
#formal_name Saccharomyces cerevisiae
19-May_1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jia, Y.K.; Becam, A.M.; Slonimski, P.P.; Herbert, C J
submitted to the EMBL Data Library, June 1995
S57724
#molecular-weight 53811 #checksum 9998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, April 1995
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98; Mismatches 125;
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##residues 1-486 ##label JIA
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##regidnes 1-43
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K.U.; Sahm, H.
Microbiology (1994) 140:1817-1828
Nucleotide sequence, expression and transcriptional analysis
of the Corynebacterium glutamicum gltA gene encoding
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Pred. No. 3.00e-33;
91; Mismatches 111; Indels 24; Gaps 20;
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                                                                                                                                                                                                           318 AAQEVVRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 ANQEVLLWIKSVVEECGENISKEQ-LKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQRE 370
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                                                                                                                                                         198 LEDSLNLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNL 257
                                                                                                                                                                                                                                                                                                                       258 TSQQSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGL 317
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16 Aug-1996 #sequence_revision 16-Aug-1996 #text_change
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#length 437 #molecular-weight 48929 #checksum 2093
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##residues 1-477 #** 1-477 #***
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Best Local Similarity 28.5%;
Matches 90; Conservative
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carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of citrate from acetyl-CoA and oxaloacetic acid tricarboxyllic acid cycle *Superfamily citrate (s1)-synthase allosteric regulation; carbon-carbon lyase; homohexamer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal J. Bacteriol. (1990) 172:2096-2104
*title Cloning of genes responsible for acetic acid resistance in Acetobacter aceti.
#cross-references MUID:90202732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 EEVIYLLLNGELPNKVQYDTFTNTLTNHTLHEQIR-NFFNGFRRDAHPMAILCGTVGAL 149
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                                               267 ALSGPLHGGANQAVLEMLEDIKSNHGGD-ATEFMNK-V-KNKEDGVRLMGFGHRVYKNYD 323
                                                                                            303 GLAGPLHGLANOEVLLWIKSVVEECGENISKEOLKDYVWKTLNSGKVVPGFGHGVLRKTV 362
                                                                                                                                              324 PRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALA-DDYFISRKLYPNVDFYTGLIYRAM 382
                                                                                                                                                                                           363 PRYTCOREFA---MKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYY 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 CIAAGIAALWGPAHGGANEAVLK-MLARIGK-KENIP-AFIAQ-V-KDKNSGVKLMGFGH 313
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249 HML-GFSS-S-EMHELLMR-L--YVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 302
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Pred. No. 1.13e-31;
85; Mismatches 111; Indels 32; Gaps
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#length 436 #molecular-weight 48196 #checksum 9071
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##cross-references GB:M34830; NID:q141729; PID:q141730
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Best Local Similarity 30.5%;
Matches 100; Conservative
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Plant Mol. Biol. (1995) 27:377-390
Molecular characterization of a glyoxysomal citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the citrate synthase of gram-negative bacteria is an allosteric enzyme whose activity is inhibited strongly and specifically by NADH
                                                                                                                                                               *authors Donald, L.J.; Molgat, G.F.; Duckworth, H.W.

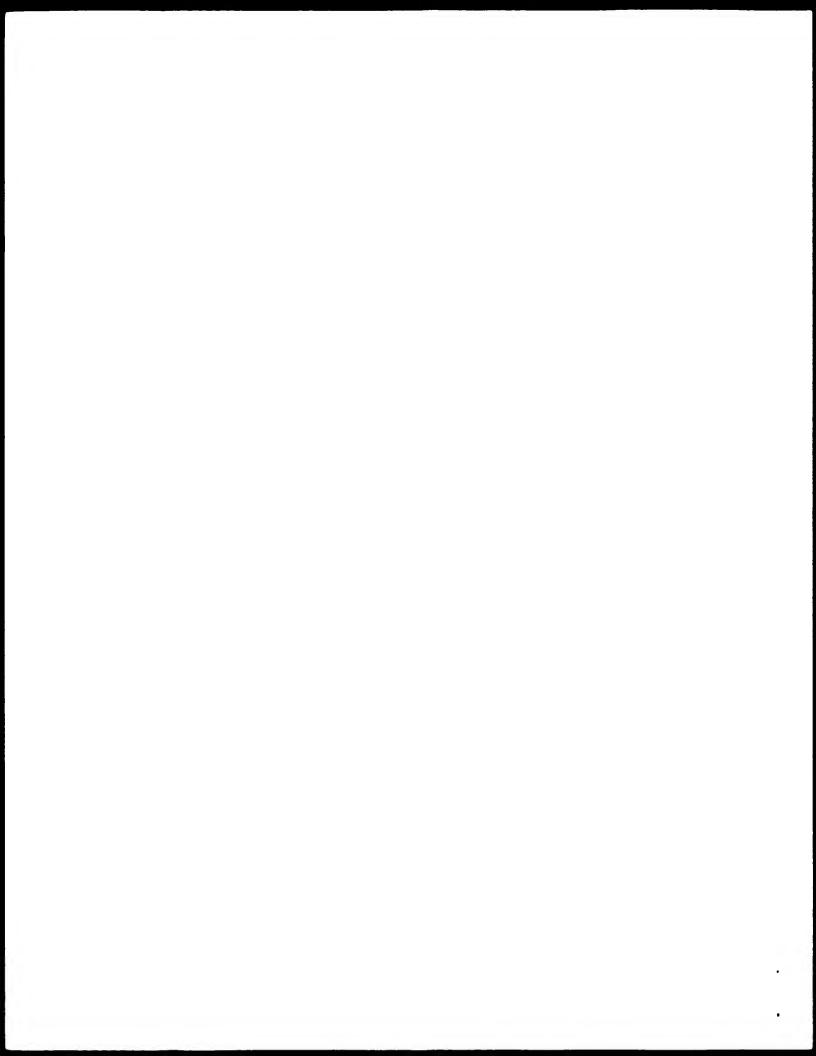
*journal J. Bacteriol. (1989) 171:5542-5550

*title Cloning, sequencing, and expression of the gene for NADH-sensitive citrate synthase of Pseudomonas aeruginosa.
YKPSCA #type complete citrate (si)-synthase (EC 4.1.3.7) - Pseudomonas aeruginosa #formal_name Pseudomonas aeruginosa 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 17-Jul-1998
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Local Similarity 27.9%; Pred. No. 1.26e-25;
les 90; Conservative 93; Mismatches 107; Indels 33; Gaps 26;
                                                                                                                                                                                                                                                                                                                                                                                                 carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 LLLNGELPTAAQKEQFVGTIKNHTMVHEQLK-TFFNGFRRDAHPMAVMC-GVIG-ALSAF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 SGIAALWGPAHGGANEAVLRMLDEIGDVSNIDKFVEKAKDKNDPFKLMGFGHRV--YKNF 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 YHDSLD--ITNPKHREVS-AHR--LIAKMPIIAAMVYK--YSKGEPMMYPRND-LNYAEN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 FLHMM-FNTPCETKPISPVLAKAMDRIFI-LHADHEQ-NASTSTVRLAGSSGANPFACIA 254
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14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change
17-Mar-1999
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#length 428 #molecular-weight 47681 #checksum 7548
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that is synthesized as a precursor of higher molecular mass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5/4344 #type complete
citrate synthase gltA - Synechocystis sp. (strain PCC 6803)
hypothetical protein sl10401
#formal_name Synechocystis sp.
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Library, June 1996
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                                                                                                                                                                                                                                                                                                                                                                    146 LLMYGNLPSQSQLADWEFAISQHSAVPQGLV-DIIQAMPHDAHPMGVLVSAMSALSVFHP 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 DANPALRGOLYKSK--QVRDKQIARIIGKAPTIAAAAYLRLAGRPPVLPSSN-LSYSEN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 EFQKAY-EKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 FAHML-GESSSE-MHEL-LMR-LYVT-I-HSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 VGALYGPLHGGANEAVLK-MLSEIGTV-NNIP-E-FIEGV-KNRKR-KM-SGFGHRVYKN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 YDPRAKVIRKLAEEVFSIVGRDPLIEVAVAL-EKAALSDEYFVKRKLYPNVDFYSGLIYR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 TVPRYTCQREFAMKHLP--E-DPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLN 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLYMLDSLGNRSYKPNPRLARVLDILFILHAEHEMNCSTSAARHLASSGV-DVFTALSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRK
                                                                                                                                                                              433 AMGFPPE-FFTVLFAIPRMAGYLAH--WRESLDDPDTKIIRPQOVYTGEWL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 516;
                                                                                                                                                                                                                                                            Score 266; DB 2; Length 516;
Pred. No. 1.33e-24;
85; Mismatches 132; Indels
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                                                                                                                                                        1-516 ##label KAT
                                                   *cross-references MUID:95195164
                                                                                                       preliminary
                                                                                                                                                                                                                                                               7.78;
                                                                                                                                                                                                                                                                                  Local Similarity 29.3%;
hes 103; Conservative
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Gaps 22;
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                                                                                                                                                                                                                                                                                                                                                                                                               57 LLIWGKLPTQAEIEEFEYEIRTHRRIKYHIR-DMMKCFPETGHPMDALQTSAAALGL--- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 LYMLTEKEPDPFAAKVFDVCLTLHAEH-TMNASTFSARVTASTLTDPYAVVASAVGTLAG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 ILQDLAEQLFAKMGHDEYYEIAVELEKVVEEYV-G-QK-GIYPNVDFYSG-LV-YRKLDI 332
#length 397 #molecular-weight 44830 #checksum 904
                                                                                                                           Ouery Match 7.6%; Score 263; DB 2; Length 397; Best Local Similarity 30.1%; Pred. No. 4.28e-24; Matches 95; Conservative 73; Mismatches 118; Indels 30;
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423 EARYYTVLFGVSRALG 438
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Search completed: Fri Oct 22 16:31:22 1999 Job time : 158 secs.



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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 16:31:39 1999; MasPar time 14.47 Seconds 920.365 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-2 (1-471) from US08702718.pep 3466 1 MVFYRSVSLLSKLRSRAVQO......PLERPKSVIMEWLENQCKKA 471 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 51.825; Variance 92.291; scale 0.562 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Query Match

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                      5;
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15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
16-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EURARYOTA, VRIDIPLANTAE, STREPTOPHYTA: EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES, SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES, BPASSICACEAE, ARABIDOPESIS.
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                                                                                                                                                                         120 EPLPEGLLWLLLTGKVPSKEQVDGLSKELRDRATVPDYV-YKAIDALPVSAHPMTQFASG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ALNGLAGPLHGLANQEVLLMIKSVVDECGENVITEQLKDYVWKTLNSGKVVPGFGHGVLR 357
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                                                                                                1 MVFYRSVSLLSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIK 60
                                                            1 MASLRSATALSRIRSRAGGGSNLSNSVPWLQMQSSADLDLHSQL-KEMIPEQQERLKKVX 59
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNGER E.A., HAND J.M., CASHMORE A.R., VASCONCELOS A.C.; "Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 FGLAEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKSVTLDWIEKNCKKA 470
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                      'n
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-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METABOLISM.
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                    56; Mismatches 41;
Best Local Similarity 78.4%; Pred. No. 0.00e+00;
Matches 371; Conservative 56; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX
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76; Indels 12; Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQS 119
                                                                                                                                                                                                                                                                                                                                                                        60 KSDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQK-VLPAAKP 117
                                                                                                                                                                                                                                                                                                                                                                                                         120 GGLNHYRRSFVASLNWKGTL-AKSKLKH-CRKTWNRAAVSDYV-YNAIDALPSTAHPMTQ 176
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                                                                                                                                                                                                                                                                     1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKKSQL-QELIPEHKDRLKKL 59
                                                                                                                                                                                                                                                                                                     1 MVFYRSVSLLSKLRSRA-VQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKI 59
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MEDLINE: 89000665.
EVANS C.T.: OWENS D.D., SUMEGI B., KISPAL G., SRERE P.A.;
"Isolation, nucleotide sequence, and expression of a cDNA encoding pig citrate synthase.";
BIOCHEMISTRY 27:4680-4686(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOKHEM D.P., PARMELEE D.C., KUMAR S., WALSH K.A., TITANI K.; "Complete amino acid sequence of porcine heart citrate synthase."; BIOCHEMISTRY 21:2028-2036(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 LNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLALERPKSVTMDWLEAHCKKA 469
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                                   HSSP; P23007; 5CSC.
LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOIA; METAZOA; CHORDAIA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                        Length 472;
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01-OCT-1989 (REL. 12, LAST SEDUBLE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                    Score 2305; DB 1;
Pred. No. 0.00e+00;
                                                                                                    CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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954AFA81 CRC32;
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                                                                                      MITOCHONDRION
 PS00480; CITRATE_SYNTHASE; 1.
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                   PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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Similarity 68.9%;
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                                                                                                                                            SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
               MEDLINE; 83010291.

REMINGTON S., WIEGAND G., HUBER R.;

"Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7-A resolution.";

J. Mol. BIOL. 158:111-152(1982).
                                                                        MEDLINE; 91104711.
ALIER G.M., CAGAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
"Mutation of essential catalytic residues in pig citrate synthase.";
BIOCHEMISTRY 29:7557-7563(1990).
-: CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                        PDB; 1CTS; 16-UUL-88.
PDB; 2CTS; 09-OCT-88.
PDB; 3CTS; 09-OCT-88.
PDB; 4CTS; 16-UUL-88.
PDB; 4CTS; 16-UUL-88.
PROSTE; PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; Citrate_Synt; 1.
LYASE: TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; 3D-STRUCTURE;
                                                                                                                                                             METABOLISM.
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                      CITRATE SYNTHASE. METHYLATION (TRI-).
        K-RAY CRYSTALLOGRAPHY (2.7 AND 1.7 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION,
                                                                                                                            PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER.
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93 DPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLIGKVPSKEQVNSIVSGIAESG 152
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                                                                                                                                                                                                                              27 SASSINLK-DILADLIPKEQARIKTFRQQHGNTVVGQITVDMMYGGMRGMKGLVYETSVL 85
                                                                                                                                                                                                                     6; Gaps
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                                                                                                                                                                                                                                                                                                                                    SDEKLRDY IWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKI
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                                                                                                                                                                                                          Score 1921; DB 1; Length 464;
Pred. No. 0.00e+00;
86; Mismatches 86; Indels 6
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Matches 254: Connection
441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE, 91255228.

LIAO D.-I., KARPUSAS M., REMINGTON S.J.;

Crystal structure of an open conformation of citrate synthase from chicken heart at 2.8-A resolution.";

BIOCHEMISTRY 30:6031-6036(1991).

-: CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                         KARPUSAS M., BRANCHAUD B., REMINGTON S.J.;
"Proposed mechanism for the condensation reaction of citrate sypthase: 1.9-A structure of the ternary complex with oxaloacetate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CITPATE SYNTHASE FAMILY.
CAUTION: THIS IS AN X-RAY DETERMINED SEQUENCE WHICH WAS
ESTABLISHED USING THE SEQUENCE OF PIG CITRATE SYNTHASE AND
MODIFYING IT MASED ON THE OBSERVED ELECTRON DENSITY.
1CSC; 15-APR-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; IAMZ; 24-DEC-97,
PROSITE; PS00480; CITRATE_SYNTHASE; 1,
PFAM; PF00285; citrate_synt; 1,
LYASE; TRICARBOXYLIG ACID CYCLE; MITOCHONDRION; 3D-STRUCTURE.
                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2 R ANGSTROMS) OF OPEN CONFORMATION
                                                                                                                01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-5UL-1998 (REL. 36, LAST SANDIATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL (EC 4.1.3.7).
                                                                                    433 AA
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                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                           and carboxymethyl coenzyme A."; BIOCHEMISTRY 29:2213-2219(1990).
                                                                                    STANDARD;
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:|||||||: : 451 LPLERPKSVTME 462
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15-APR-91.
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24-DEC-97.
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30-APR-94.
15-OCT-95.
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MEDLINE; 90248434.
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PDB: 2CSC;
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PDB: 5CTS;
PDB: 5CTS;
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94 PDEGIRFRGLSIPECOKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGI 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 IAQVPLVAAYVYRRMYKNGDTI-PKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 PNVLLEQGAAANPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PDEGIRFRGFSIPECQKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 LPSHVV-TMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DASLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCOREFALKHLPGDPMFKLVAQLYKIV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ASSTNLK-DVLAALIPKEQARIKTFRQQHGGTALGQITVDMSYGGMRGLVYETSVLD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                       35 SSGLDLRSELVQELIPEQQDRLKKIKSDMKGS-IGNITVDMVLGGMRGMTGLLWKPHYLD 93
                                                                                                                                                                                                                                                                                                                                                                                     Score 1842; DB 1; Length 433;
Pred. No. 0.00e+00;
85; Mismatches 94, Indels 6, Gaps
                                                                                                                                                                                                                                                                                                                                                                    47373 MW; 6E24FE58 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                     / Match 53.1%;
Local Similarity 57.1%;
hes 246; Conservative
343
364
365
372
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375
385
390
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427
433 AA;
345
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METABOLISM.
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                                                                                                                                                                                       LT 6
CISY_SCHPO
Q10306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                               --- PATHWAY: TPICAPBOXYLIC ACID CYCLE.
--- SUBUNIT -- HOMODIMBR (BY SIMILABITY)
--- SUBCELLULAR LOCATION- MITOGENERAL MATRIX (BY SIMILARITY)
--- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM: PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
HYPOTHETICAL PROTEIN; LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 NARADLPTHVV-RMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 AESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 TSVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEW 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 DSMDLLAKLPTVAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAEL-MRLYL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 VIHSDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 LSTSAEGSTNLKEVLSKK-IPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 LQVQTSSGLDLRSELVQELIPEQQDRLKKIKSDMKGSIG-NITVDMVLGGMRGMTGLLWK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00e+00;
84; Mismatches 109; Indels 8; Gaps
                                                                                                                                   CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                       01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PPOBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 468;
                                                                                                                                                                                                                          SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
(), ADA3A630 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1722; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WORMPEP; T20G5.2; CE00513.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 49.7%;
Local Similarity 54.0%;
les 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z30423; G458482; -.
                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
468
303
349
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452 PLERPKSVTME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $42370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 AA;
                                                                                                                                                                                                STRAIN=BRISTOL N2:
BERKS M., SMITH A.
SUBMITTED (MAR-199
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303
349
404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSIT PEPTIDE
                                                                                                                                                                                                                                                                                                                 METABOLISM
                                              CISY_CAEEL P34575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 RFRGYIIPECQKLLPSSPNGKQPLPESLFWLLVTGEIPTLSQVQALSADWAARSQLPKFV 169
                                                                                                                                                                                                                    382 LYKITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIW 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 LKDRLA-ELIPEKQAEIKKFRAEHGQDVIGEVTINQMYGGARGVRSLIWEGSVLDPNEGI 109
268 TIHSDHEGGNVSAHTGHLVASALSDFYLSFAAALNGLAGFLHGLANQEVLLWIKSVVEEC 327
                                                                                                                                                       328 GENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN; LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYIIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O + OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 LRSELVQELIPEQOBLLKKIKSDM+KGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                           322 GFNYTEEQLKEWVWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHOMORIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MITOCHONDRION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.00e+00;
83; Mismatches 101, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITRATE SYNTHASE.
BY SIMILARITY
BY SIMILARITY.
BY SIMILARITY.
7; 18145A7D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1716; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00480; CITRATE_SYNTHASE; 1. PFAM; PF00285; citrate_synt; 1. HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54030 MW;
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es 237; Conservative
                                                                                                                                                                                                                                                                                                                                                     441 ARGMGLPLERPKSHSTD 457
                                                                                                                                                                                                                                                                                                                                                                                                              446 DRALGLPLERPKSVTME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z69731; E223710; -.
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319
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365
420
482 AA;
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PATHWAY: TRICAPBGXYLIC ACID CYCLE SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
170 E-ELIDRCPPTLHPMAQFSLAVTALEHDSAFAKAYERGMNKHDYWKYEYEDCMDLIAKTV 228
                                    159 MYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVP 218
                                                                                                                 219 LVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNV 278
                                                                                                                                                     289 SAHTGHLVGSALSSPFLSMAASLNGLAGPLHGLANQEVLNFLITMKKEIGDDLSEETIKS 348
                                                                                                                                                                                          279 SAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKD 338
                                                                                                                                                                                                                                                                                                                               399 LAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPK 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEBHASSELT P , AERT R., VOET M , VOLCKAERT G.; "Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right
                                                                                                                                                                                                                                                    229 PIAGRIYRNLYRDGVVAPIQMDKDHSYNFANVLGFANNEEFVELMRLYLTIHADHEGGNV
                                                                                                                                                                                                                                349 YLWKLLNSGRVVPGYGHAVLRKTDPRYTAQREFALEHLPKDPMFQLVSPLYEIVPGVLTE
                                                                                                                                                                                                                                                                                                         409 HGKTKNPYPNVDSHSGVLLQYYGLKEQSFYTVLFGVSRTLGVASQLIWDRALGLPIERPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITCHONDETAL PRECURSOR (EC 4.1.3.7).
CITL OR LYSS OF SLUI OF YNROULC OR N2019.
SACCHAROWYCES CEREVISIAE (BAREY'S YEAST).
EUKARYOTA, FUNGI, ASCOMYCOTA, HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETAGEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening method "; EMBO J 3:1773-1781(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Organization of the centromeric region of chromosome XIV in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAST 10:523-533(1994).
-!- CATALYTIC ACTIVITY· CITPATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STETTLEP S , MARIOTTE S., GENDREAU E , THURIAUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (JUL-1993) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUISSA M., SUDA K., SCHATZ G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-D273-10B;
LINDNER P., PLUECKTHUN A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EAST 10-1355-1361(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 85003587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                      469 SFSTE 473
                                                                                                                                                                                                                                                                                                                                                                                                                          458 SVTME 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 IISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFOKAYEKGIHKSKYWEPTYEDSMN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 LLGKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDL-MRLYLTIHSD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 HEGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 PGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 LLFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 DPEEGIRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 DPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 LIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 KETIEKYLWDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVST1YEVA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 TSSGLDLRSELVQELIPEQQDRLKKIKSDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION: TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.00e+00;
90; Mismatches 106; Indels
SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITRATE SYNTHASE.
BY SIMILARITY
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E -> O (IN REF. 2).
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W; C6896385 CRC32;
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NO. 0.00c+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00480; CITRATE_SYNTHASE; 1.
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HSSP; P23007; 5CSC.
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Conservative
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EMBL; X77395; G496718; -.
EMBL; Z71616; E239778; -.
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PIR; S35390; S35390.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 LLTGEVPSEQOVRDLSAEWAARSDLPKFIE-ELIDRVPSTLHPMAQFSLAVTALEHESAF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 AKATAKGINKKDYWNYTFEDSMDLIAKLPTIAAKIYRNVFKDGKVAPIQKDKDYSYNLAN 250
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                                                                                                                                                                                                                                                                                                              MEDLINE; 97306446.

PARK B.W., HAN K.H., LEE C.Y., LEE C.H., MAENG P.J.;

Pack B.W., HAN K.H., LEE C.Y., LEE C.H., MAENG P.J.;

Factoring and characterization of the cata gene encoding the mitochodrial citrate synthase of Aspergillus nidulans.";

MOL. CELLS 7:290-295(1997).
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                                                                                                        EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA: FUNGI: ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; EMERICELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION (POTENTIAL).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
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SY SIMILARITY.
D97E1E91 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             larity 54.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U89675; G2138332; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA;
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                                                                                                                                                                                                                                                                                           STRAIN-FGSC 4;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 SDLPKFIE-ELIDRCPSTLHPMSQFSLAVTALEHESAFAKAYAKGINKKDYWNYTFEDSM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 DLIAKLPTIAAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGYGDNNDFVELMRLYLTIHS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 DHEGGNVSAHTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTKMKAAIGNDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 DSEEGIRFRGRTIPECQELLPKA-PGGQEPLPEGLFWLLLTGEIPTEQQVRDLSAEWAAR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 NLIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 DHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 TSSGLDLRSELVQELIPEQQDRLKKIKSDMKGS-IGNITVDMVLGGMRGMTGLLWKPHYL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 TGKAKSLKETFAEKL-PAELEKVKKLRKEHGSKVIGEVTLDQAYGGARGVKCLVWEGSVL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 DPDEGIRFRGLSIPECOKVLPAAKPGG-EPLPEGLLWLLIGKVPSKEQVNSIVSGIAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSHIDA Y., MIYAKE K., KANAYAWA S., KIRIMURA K., USAMI S.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRION (BY SIMILARITY) CITRATE SYNTHASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                              01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4 1.3 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 48D237BC CRC32;
                                   430 TVLFGVSRALGVLPQLIIDRAFGAPIERPKSFSTE 464
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                                                                                                                                                                                                                                                          (REL. 34, CREATED)
(REL. 34, LAST SEQU
(REL. 34, LAST ANNO
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Local Similarity 54.9%;
les 237, Conservative
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                                                                                                                                                                                                     STANDARD;
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356
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ASPERGILLUS NIGER.
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356
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01-0CT-1996 (
01-0CT-1996 (
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                  P51044;
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                                                                                                                                                                                                     SOLUTION STATEMENT OF STATEMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITRATE SYNTHASE IS FOHND IN NEAPLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                392 FLLFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 SDEAIKNYLWSTLNAGQVVPGYGHAVLRKTDPRYVSQREFALRKLPDDPMFKLVSQVYKI 392
                                      332 SKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEV 391
                                                                            393 APGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEANYYTVLFGVSRALGVLPQLIIDRALG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 EQAYGGMRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLPEALFWLLT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 DMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 GEVPTEAQTRALSEEFAARSALPKHVE-ELIDRSPSHLHPMAQFSIAVTALESESQFAKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RSSNVAKSTLKNSVR--TYATAEP-TLKQRL-EEILPAKAEEVKQLKKDYGKTVIGEVLL 64
                                                                                                                                                                                                                                                                                                                                                                                                                          FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE TRANSIT 1 PATIOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UEDA M., SANUKI S., KAWACHI H., SHIMIZU K., ATOMI H., TANAKA A. SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1639; DB 1; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION (POTENTIAL).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                    CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                     457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS00480; CITRATE_SYNTHASE; 1. PFAM: PF00285; citrate_synt; 1. HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                         01-NOV-1997 (PEL. 35, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 402 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB001565; G1871439; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.38;
                                                                                                                                                                                                                                                                                                                                                                                                      CANDIDA TROPICALIS (YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                     STANDARD;
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301
                                                                                                                                                                                           451 LPLERPKSVTME 462
                                                                                                                                                      453 APIERPKSYSTE 464
                                                                                                                                                                                                                                                                                                                                                                                                                                        CANDIDACEAE; CANDIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-PK233;
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                                                                                                                                                                                                                                                                   CISY_CANTP
P79024;
                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
ACT_SITE
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITERATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
184 YAKGVHKSEYWKYTYEDSIELLAKLPTIAAKIYRNVFHDGKLPAQIDSKLDYGANLASLL 243
                                                                            302
                                                                                                              252 GFSSS-EMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHG 310
                                                                                                                                                  RANQEVLEWLFKLREELNGDYSKEAIEKYLWDTLNAGRVGPGYGHAVLRKTDPRYTAQRE 362
                                                                                                                                                                                         311 LANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQRE 370
                                                                                                                                                                                                                               363 FALKHMPDYELFKLVSNIYEVAPGVFDQHGMTK-NPWPNVGSHSGVLLQYYGLTEESFYT 421
                                                                                                                                                                                                                                                   FEREA I., CONTRERAS E.T., OUNG T., BOWMAN E.J., ROWMAN B.J.;
"Characterization of the out-1 gene from Neurospora crassa encoding
the mitochondrial form of citrate synthase.";
MOL. GEN. GENET. 242:105-110(1994).
-!- CATALYTIC ACTIVITY: CITRATE + GOA = ACETYL-GOA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION- MITOCHONDRIAL MATPIX.
-!- DEVELOPMENTEL STAGE: ABUNDANT AFTER 6-12 HRS OF GROWTH. IT IS
NOT SIGNIFICANTLY EXPRESSED AFTER 24 HRS, WHICH IS SEVERAL HRS
AFTER ENTERING THE STATIONARY PHASE OF GROWTH.
                      244 GFGENKEFLEL-MRLYLTIHSDHEGGNVSAHTTHLVGSALSSPFLSLAAGLNGLAGPLHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTION UPDATE)
CITRALE SYNTHASE, MITOCHONDPIAL PRECURSOR (EC 4 1 3 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCHONDRION (POTENTIAL) CITRATE SYNTHASE.
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                                                                                                                                                                                                                                                                                                       422 VLFGVSRAFGVLPQLILDRGLGMPIERPKSFSTE 455
                                                                                                                                                                                                                                                                                                                                429 VLFGVSRALGICSQLIWDRALGLPLERPKSVTME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00480: CITRATE_SYNTHASE; 1. PFAM: PF00285; citrate_synt; 1. HSSP; P23007; SCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SORDARIALES; SORDARIACEAE; NEUROSPORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------
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                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
469
352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROSPORA CRASSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                    CISY_NEUCR
P34085;
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46.3%; Score 1606; DB 1; Length 469;

Query Match

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               6
                                                                                                                                                                                                   222 YQNVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELL-RLYLJIHTDHEGGNVSAHTT 280
                                                                                                                                                                                                                                                        281 HLVGSALSSPFLSVAAGLNGLAGPLHGLANQEVLNWLTEMKKVIGDDLSDEAITKYLWDT 340
                                                                                                                                                                                                                                                                                                             341 LNAGRVVPGYAHAVLRKTDPRYSAQRKFAQEHLPEDPMFQLVSQVYKIAPKVLTEHGKTK 400
                                      44 ELLPENIEKIKALRKEHGSKVVDKVTLDQVYGGARGIKCLVWEGSVLDAEEGIRFRGKTI 103
                                                               47 ELIPEQODRLKKIKSDMKGSI-GNITVDMYLGGMRGMTGLLWKPHYLDPDEGIRFRGLSI 105
                                                                                                         162 RCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLPTIAARI 221
                                                                                                                                                                                                                            225 YRRMYKNGDTIPKDESLDYGANFAHMLGFSSS-EMHELLMRLYVTIHSDHEGGNVSAHTG 283
                                                                                                                                                                                                                                                                                284 HLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKT 343
                                                                                                                                                                                                                                                                                                                         401 NPYPNVDAHSGVLLQHYGLTEANYYTVLFGVSRAIGVLPQLIIDRAVGAPIERPKSYSTD 460
                                                                                                                                                                                                                                                                                                                                                                                 104 PECQELLPKA-PGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKFIE-ELID 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mitochondrial and nonmitochondrial citrate synthases in
Saccharomyces cerevisiae are encoded by distinct homologous genes.";
MOL. CELL. BIOL. 6:4509-4515(1986).
               9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92254505.

BITEAU N., FREWAUX C., HEBRARD S., MENARA A., AIGLE M., CROUZET M.; The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae."; YEASI 8:61-70(1992).
                                                                                                                                                                SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNG1; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIAO.X., SMALL W.C. SPEPE P.A., BUTOW R.A.;
LIAO.X., SMALL W.C. SPEPE P.A., BUTOW R.A.;
"Intramitochondrial functions regulate nonmitochondrial citrate synthase (CIT2) expression in Saccharomyces cerevisiae.";
MOL. CELL. BIOL. 11:38-46(1991).
-!- CATALYIIC ACTIVITY CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSENKRANTZ M., ALAM T., KIM K.-S., CLARK B.J., SRERE P.A.,
              79; Mismatches 106; Indels
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (FEL 06, CPEATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITATRE SYMTHASE, PEROXISOMAL (EC 4.1.3.7).
CIT2 OR YCR005C OR YCR5C OR YCR043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; FUNGI; ASCOMYCOTA; HEMI
SACCHAROMYCETACEAE; SACCHAROMYCES.
Best Local Similarity 54.8%;
              235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-24 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                       461 KWIEI-CKK 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CISZ_YEAST
P08679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
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              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 GLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLTGKVPSKEQVNS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 IVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 SYTFEDSLDLLGKLPVIAAKIYRNVFKDGKMGEVDPNADYAKNLVNLIGSKDEDFVDL-M 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 RLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSV 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 VEECGENISKEQLKDYVWYTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 GSVWEGSVLDPEDGIRFRGRTIADIQKDLPKAKGSSQPLPEALFWLLIGEVPTQAQVEN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 LSADLMSRSELPSHVV-QLLDNLPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLYLTIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEVLEWLFAL 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 LVSSIYEVAPGVLTEHGKTKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQ 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 NVASYLQSNSSQEKTLK-ERFSEIYPIHAQDVRQFVKEHGKTKISDVLLEQVYGGMRGIP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 NSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKK-IKSDMKGSIGNITVDMVLGGMRGMT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

BY SIMILARITY.

MICROBODY TARGETING SIGNAL (POTENTIAL).

9E93E2FD CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEROXISOME; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93; Mismatches 120; Indels
                                                          SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 45.4%; Score 1575; DB 1; Similarity 50.5%; Pred. No. 0.00e+00;
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01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; L0000342; CIT2.
PROSITE; PS00342; MICROBODIES_CTER; 1.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYASE; TRICARBOXYLIC ACID CYCLE;
ACT_SITE 293 293 BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 AA; 51413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 LIWDRALGLPLERPKSVIME 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 LITDRAIGASIERPKSYSTE 447
                                                                                                                                                                                                                                                                                                                                                                           EMBL; M14686; G171227; -.
EMBL; M54982; G171229; -.
EMBL; X59720; E264468; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                EMBL; Z11113; G3299; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339
394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A25393; YKBYC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P23007; 5CSC
                              METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CISY_TETTH P24118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
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381 DVIPKKLLTYKKIANPYPNYDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSR 439
381 DVIPKKLLTYKKIANPYPNYDCHSGVLLYSLGLTERYYTVLFGVSRALGIC-SGLIWPP 447
390 EVFLLELQNIARL FROPPNYDAHSGVLLYYGLTERRYYTVLFGVSRALGIC-SGLIWPP 447

440 AFGLPIERPGSADLKWFHDKYR 461

g

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330 NISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLY 389

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95; Mismatches 124; Indels 16; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 GIIFRGYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 GIRFRGLSIPECQKVLP-A-AKPG--G--EPLPEGLLWLLLTGKVPSKEQVNSIVSGIAE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 RGTVNQDCVNFILN-LPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYED 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 SMDLIAKIPRVAAIIYPHKYPDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECI-RGYLSI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 HSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGE 329
                                                                                    EUKARYOTA; ALVEOLATA; CILIOPHORA, OLIGOHYMENOPHOREA; HYMENOSTOMATIDA,
TETPAHYMENINA; TETRAHYMENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 DLRSELVQELIPEQQDRLKKIKSDMKGSI-GNITVDMVLGGMRGMTGLLWK-PHYLDPDE 96
                                                                                                                                                                                                                                                                                                                                                                                                                  BIOCHEM. BIOPHYS. RES. COMMUN. 174:1028-1034(1991).
-!- FUNCTION: STRUCTURAL PROTBIN INVOLYED IN ORAL WORPHOGENESIS AND
IN PRONUCLEAR BEHAVIOR DURING CONJUGATION. RESPIRATORY ENZYME.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL.COA + H(2)O +
                                                                                                                                                                                                                                                     NUMATA O., TAKEMASA T., TAKAGI I., HIRONO M., HIRANO H., CHIBA J., WATANABE Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:||| :| ||| :||:||:||:|| || || :||:|||:||
210 SMNLIAQVPLVAAYVYRRMYKNGDIIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 NLKK-VIAEIIPQKQAELKEVKEKYGDKVVGQYTVKQVIGGMRGMKGLMSDLSRC-DPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 SGIISLIIMYTTIDALPVTAHPMIQFATGVMALQVQSEFQKAYEKG-IHKSKYWEPTYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 HCDHEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGT
                                                                                                                                                                                                                                                                                                                                                'Tetrahymena 14-nm filament-forming protein has citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION· MITOCHONDRIAL MATRIX AND CYTOPLASMIC
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 8.03e-269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITCCHONDRION
                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 22-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JN0130; JN0130.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt; 1.
HSSP; P23007; SCSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h
Similarity 46.8%;
                                    FILAMENT-FORMING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90117; E33571; -.
                                                                     TETRAHYMENA THERMOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOSKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOSKELETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                         activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
SOURCE SERVING COURSE CONTRACTOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ά
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITPATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRICARBOXYLIC ACID CYCLE; MULTIGENE FAMILY.

IE 315 315 BY SIMILARITY.

IE 361 BY SIMILARITY.

IE 419 419 BY SIMILARITY.

484 486 MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                               01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHAGE 3 (SCC 4.1.3.7).
CITRATE SYNTHAGE 3 (SCC 4.1.3.7).
CITRATE SYNTHAGE (BAKER'S YEAST).
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                 PEARSON D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                    WANG Y., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D., HALL J. STOWNS R.K., VO D.H., WINNETT E.; SUBMITTED (XXX-1995), TO EMEL/GENBANK/DBJ DATA BANKS.

-1. CATALITIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METABOLISM.
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                             JIA Y.K., BECAM A.-M., SLONIMSKI P.P., HERBERT C.J.; SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 3.93e-231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       806F987D CRC32;
   486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00342; MICROBODIES_CTER; PROSITE; PS00480; CITRATE_SYNTHASE;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                          SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00285; citrate_synt; 1.
HSSP; P23007, 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53811 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X88846; G895889; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 248951; G763000; -.
EMBL; 271255; E236811; -.
EMBL; U31900; G939735; -.
   STANDARD;
                                                                                                                                                                                                                                                                                                 STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; L0002855; CIT3
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 207;
                                                                                                                                                                                                                STRAIN-CW04;
CISX_YEAST
P43635:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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21 IIKSSALTIKEAL-ENVIPKKRDAVKKLKACYGSTFVGPITISSVLGGMPGNQSMFWQGT 79

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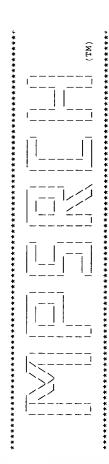
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: TRICARBOXYLIC ACID CYCLE.
SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                 80 SLDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELA 139
                                                                                    91 YLDPDEGIRFRGLSIPECQKVLPAAKPGGEP-LPEGLLWLLJIGKVPSKEQVNSIVSGIA 149
                                                                                                                                   140 IRGR-KLPH-YTEKVI,SSLPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDT 197
                                                                                                                                                          198 LEDSLNLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMINGTNSSNTCNL 257
                                                                                                                                                                                                                                        207 YEDSMNLIAQVPLVAAYVYRRMYKNGDTIPK-DESLDYGANFAHMLGFS----SSE---M 258
                                                                                                                                                                                                                                                                                            258 TSQQSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGL 317
                                                                                                                                                                                                                                                                                                                             259 --HE-L---LMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGL 311
                                                                                                                                                                                                                                                                                                                                                                        318 AAQEVVRFIJEMNSNIS-STAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 FAQKRPIEFENDKNVLLMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLF 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 FAMKH-LP-E-DPLFQLVSKLYEVFLLFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIKMANNS B.J., THUM-SCHMITZ N., EGGELING L., LUEDTKE K.U., SAHM H.; "Nucleotide sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase."; MICROBIOLOGY 140:1817-1828(1994).
ENZYME REGULATION: WEAKLY INHIBITED BY ATP (APPARENT KI = 10 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; CORYNEBACTERIACEAE;
CORYNEBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 FTVIFGCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CISY_CORGL STANDARD; PR. P42457; 01-NOV-1995 (REL. 32, LAST SEQUE: 01-NOV-1995 (REL. 32, LAST SEQUE: 01-NOV-1995 (REL. 32, LAST ANNOT CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORYNEBACTERIUM GLUTAMICUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=ATCC 13032;
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PROSITE; PS00480; CITRATE\_SYNTHASE; 1. PFAM; PF00285; citrate\_synt; 1. HSSP; Q53554; 1AJ8.

EMBL; X66112; G505581; -.

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Pred. No. 2.97e-39;
91; Mismatches 111; Indels 24; Gaps 20;
                                                                                                                                                                                                                                                       97 LLINGELPTPDELHKFNDEIRHHTLLDEDFK-SQFNVFPRDAHPMATLASSVNILST-Y- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ-NCSTSTVRMIGSAQANMFVSIAGGIN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 HML-GFSS-S-EMHELLMR-L--YVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLRKTV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 PRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALA-DDYFISRKLYPNVDFYTGLIYRAM 382
                                                                                                                                                                                                                                                                                                            129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
                                                                                                                                                                                                                                                                                                                                                                                                                        189 FQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 ALSGPLHGGANQAVLEMLEDIKSNHGGD-ATEFMNK-V-KNKEDGVRLMGFGHRVYKNYD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 PRYTCQREFA---MKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYY 419
                                                                                                                                                                                                                                                                                                                                                                   154 YQDQLN-PLDEAQL-D-K--ATVRLMAKVPMLAAYAHRAR-KGAPYMYPDNSLNARENFL 207
                                                                                                                                              DB 1; Length 437;
LYASE; TPICARROXYLIC ACID CYCLE; ALLOSTERIC ENZYME. ACT_SITE 316 316 BY SIMILARITY. ACT_SITE 372 372 BY SIMILARITY. SEQUENCE 437 AA; 48929 MW; B408BFAS CRC32;
                                                                                                                                              Score 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: Fri Oct 22 16:32:36 1999 Job time : 57 secs.
                                                                                                                                         9.1%;
Local Similarity 28.5%;
nes 90; Conservative
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                                                                                                                                              Query Match
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Sat Oct 23 15:30:25 1999; MasPar time 3195.79 Seconds 1386.485 Million cell updates/sec Run on:

n.a. - n.a. database search, using Smith-Waterman algorithm

MPsrch\_nn

Tabular output not generated.

Title:

>US-08-702-718-1 (1-1891) from US08702718.seq 1891 Description: Perfect Score: N.A. Sequence:

1 TITITGGTTGCATCAGCCTA.......TTATTTGATGATATTATGAA 189... AAAAAGCAAGGTAGTGGGAT......AATAAACTACTATAATACTT

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD : Nmatch

2883791 seqs, 1171580779 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Database:

1:em\_est10 2:em\_est11 3:em\_est17 4:em\_est18 5:em\_est2
6:em\_est9 7:em\_gss1
genbank-est111 embl-est58

8:qb\_est1 9:qb\_est10 10:qb\_est11 11:qb\_est12 12:qb\_est13 13:qb\_est14 14:qb\_est15 15:qb\_est16 16:qb\_est17 17:qb\_est18 119:qb\_est2 20:qb\_est27 21:qb\_est21 22:qb\_est22 23:qb\_est2 20:qb\_est23 24:qb\_est24 25:qb\_est25 26:qb\_est26 27:qb\_est27 28:qb\_est28 33:qb\_est28 33:qb\_est28 33:qb\_est8 33:

Mean 11.716; Variance 1.945; scale 6.023

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

			ф					
Result No.	No.	Score	Query Match	Query Match Length DB ID	DB	GI GI	Description	Pred. No.
!	; 	241	12.7	471	20	AA896953	L30-386T3 Ice plant La	0.0000
	C4	200	10.6	203	17	T44185	7448 Lambda-PRL2 Arabi	0.00e+00
	m	189	10.0	478	31	R90544	16899 Lambda-PRL2 Arab	0.00e+00
	4	179	9.5	620	56	AU002699	AU002699 Bombyx mori p	0.00e+00
	Ŋ	172	9.1	417	24	C96653	C96653 Rice callus Orv	0.00e+00
ပ	9	173	9.1	929	23	AI176862	EST220465 Normalized r	0.00e+00
	7	153	8.1	657	15	AA606966	vm94h09.rl Knowles Sol	3.25e-287
	œ	150	7.9	307	10	AA231705	CDO534.R cDNA from oat	5.79e-280
	σ	150	7.9	527	31	R90561	16916 Lambda-PRL2 Arab	5.79e-280
	10	144	7.6	501	11	AA313713	EST185581 Colon carcin	1.68e-265

2.69e-246 4.57e-220	3e-20	.02e-19	.91e-19	.02e-19	.42e-18	.25e-17	.46e-17	.46e-17	.12e-17	2e-17	.12e-17	.12e-17	.03e-16	e-16	.13e-16	.94e-15	3.64e-152	.44e-14	.27e-15	4e-14	.27e-15	7e-15	.83e-14	3e-14	.83e-14	.05e-13	5e-13	.05e-13	.34e-13	.34e-13	e-13	.54e-12	.65e-12
r1	9b06.rl Stra	17 Lambda-FRL2 Ar	000	8gll.rl Barstea	5054.5prime GH D	th09.rl	08g10.rl Soares	6a01.s1	5e02.rl Soares	8d01.s1	6h01.rl Soares m	mt23d11.rl Soares mous	ST36505 Embryo, 8	2223	8q03.s1	3.rl Stratag	2ZA101 r	yx90c03.rl Soares mela	265 Yuji Kohara	c01.r1 So	-R-A1-dp-g-06-0-	820 Dictyo	27941 Cerebellu	4h04.r	fl0.xl Soares	54627 Jurka	9h09.rl Stra	554 Rice callu	r00324 Maize Lea	89c01.s1	ST24544 Ce	11 Ch	88687 Mou
AA237580 217455	1294	72022	548	49829	3891	5	121	0	36	3095	7872	7742	325	3746	9254	19693	159	572	C13265	4271	0122	32	2501	9203	27	5612	9693	55	36	3298	7	33	9
522 10 213 8	66 3	52 1	85 2	73 1	40 2	42 3	44 1	89 2	18 3	94 1	03	60	31 1	38 I	43 2	52	21 1	58 3	60 3	55 1	06 2	42 1	65 1	04	52 2	02 1	19	68 2	91 3	31 1	37 1	06	10 2
7.2								٠				٠									٠			٠		4.8	٠	4.8		•	•	4.5	4.5
136 125	120	115	116	113	109	105	106	106	104	104	104	104	101	101	100	86	96	94	95	94	92	95	66	66	66	06	06	06	88	88	88	98	82
11					17	18	19	c 50	21	c 22	23	24	25	56	27	28	53	30	31	32	c 33	34	35	36	c 37	38	36	40	41	42	43	44	45

# ALIGNMENTS

1 AA896953 471 bp mRNA EST 06-APR-1998 N L30-386T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaC1 treatment Mesembryanthemum crystallinum cDNA clone L30-386 5' similar to Citrate synthase, mitochondrial precursor, mRNA	×		Contact: Cushman JC Department of Biochemistry and Molecular Biology Oklahoma State University 350 Noble Research Center, Stillwater, OK 74078-3035, USA Tel: 405-744-6207 Faz: 405-744-7799 Email: jcushman@blochem.okstate.edu PCR PRimers FORMARD: T7 BACKWARD: T3 Plate: L30.4 row: H column: 6 Seq primer: T3
RESULT LOCUS DEFINITION	ACCESSION NID VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	

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ACCESSION
                                                                                                                                                                                                                   FEATURES
    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes: Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae: Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 502)
                                                       /organism="Mesembryanthemum crystallinum"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1102 TTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGCAGATTCTGCGAAAGACTGTACCA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          982 TTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATAAAATCTGTT 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 AGATACTCTTGCCAGAGGGACTTTGCCCTTAAGCACTTACCTAATGATCCACTATTTCAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TTGGCTGGCCCACTTCATGGATTAGCCAATCAGGAAGTGTTGCTGTGGATCAAGTCAGTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 GTGGATGAATGTGGAGAAACATCAGCACGGAGCAGCTAAAAGATTATGTCTGGAAGACA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 TTAAAAAGTGGCAAGGTTGTACTGGATATGGCCATGGAGTTCTGCGCAAGACGGATCCA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 CIGGITICGAAGCIGIAIGAAIGGIGCCICCAATICTGACAGGGGGAAGGIAAAGA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T44185 502 bp mRNA EST 07-JAN-1998
7448 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123C9T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 ACCATGGCCGAATGTTGATGCCCACAGTGGGTGTATTGCTGAACTACTATGGTTTGACAA 422
                                                                                                                                                                                                                                                                                                                                                                                              922 CACTIGGITGCTAGIGCTITGTCTGAICCTTACCICTCCTTIGCTGCTGCTTIGAATGGT 981
                                                                                                                                                                                                                                                                                                                                                                        3 CATTTGGTGGGTAGCGCACTTTCAGATCCTTACCTTTCATTTGCAGCTGCACTGAATGGG 62
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                  /close_lb="loe plant Lambda Uni-Zap XR expression
library, 30 hours NaCl treatment"
/tissue_type="leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
195 c 122 q 127 t
                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                             Score 241; DB 20; Length 471; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                   0; Mismatches 86;
High quality sequence stop: 320.
Location/Qualifiers
                                                                                                              /db_xref="taxon:3544"
/clone="L30-386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1339 GAA-GCAAGATATTATACGGT 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 GAAAGCAAGATACTACACTGT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                             Query Match 12.7%;
Best Local Similarity 79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r44185.1 GI:2758988
                                                                                                                                                                                                                                                                                                                                   351; Conservative
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SOURCE
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/strain-war columbia zip Lox; Site_1: Sal, Site_2: Not, Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA inserts were directionally cloned with Sal-Not arms using
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DEFINITION 16899 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189D15T7, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
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On Jan 7, 1998 this sequence version replaced gi:948518
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Pred. No. 0.00e+00;
0; Mismatches 74; Indels
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90 c 118 g 149
                                                                                       MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                        Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7.
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                                                           Contact: Thomas Newman
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Best Local Similarity 79.1%;
Matches 291; Conservative
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KEYWORDS
SOURCE
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AU002599.1 GI:4159092
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Genome Research Group
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Best Local Similarity 66.4%;
Matches 392; Conservative
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// Strain-"var columbia"
// Note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
// Lambda PRL2 is a cDNA library derived from equal
// Lambda PRL2 is a cDNA library derived from equal
// Apools of mRNA. The mRNA sources were 1)
// day germinated etiolated seedlings; 2) tissue culture
// grown roots; 3) staged plants half with 24 hour light
// Same plants as 3 but aerial issue (stems, flowers and
// sliques. The vector is BRL's lambda Zip-Lox. The CDNA
// Inserts were directionally cloned with Sal-Not arms usin:
// Apools of the columbia columbia columbia columbia columbia columbia columbia columbia columbia.
                                                                                                                                                           large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
                                                                                                 Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, F. and Somerville, C. Genes galore: a summary of methods for accessing results from
                 Eukaryota, Viridiplantae, Streptophyta: Embryophyta: Tracheophyta euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae: Capparales; Brassicaceae; Arabidopsis.

[ (bases 1 to 478)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ATATCAAAAGAACAGTIGAAAGAATATGTTTGGAAAACATTAAACAGTGGCAAGGTTATT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 ITGGCTAATCAGGAAGTTTTGCTTTGGATCAAATCAGTCGTAGAGGAATGTGGAGAAGAT 123
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                                                                                                                                                                                                                                                                                                         MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
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Pred. No. 0.00e+00;
C; Mismatches 66; Indels
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90 c 113 q 13
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
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Location/Qualifiers
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RESULT

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AU002699 620 bp mRNA EST 15-JAN-1999
AU002699 Bombyx mori p50(Daizo) Bombyx mori cDNA clone n0357, mRNA
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                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Lepidoptera, Bombycoidea, Bombycidae, Bombyx.
1 (bases 1 to 620)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Establishment of cDNA database of Bombyx mori
Unpublished (1999)
on Sep 1, 1995 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 179; DB 26; Length 620; Pred. No. 0.00e+00;
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141 c 146 g 171 t
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PROJECT - 'CREST project by JST'.
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/db_xref="taxon:7091"
/clone="n0357"
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Oryza sativa
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes: Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="cultivar Nipponbare, sub_species Japonica"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dI) as a primer and ligating to the SalI-Noti site
of pBluescript II SK+ phagemid. "
/db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 ATGCGACTATATGTGACAATCCACACTGATCATGAAGGTGGAAATGTCAGTGCTCATACT 178
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                                                                                                                                                    19-0CT-1998
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                                                                                                                                               LOCUS C96653 417 bp mRNA EST 19-OCT-19
DEFINITION C96653 Rice callus Oryza sativa cDNA clone C10531_5A, mRNA
                                              1423 TIGCCGCTAGAGAGGCCAAAGAGTGTCACAATGGAGTGGCTTGAGAACCA 1472
  541 CTTCCCATTGAGAGACCAAAGTCGCTCAGCACGGAGATGCTTATGAAACA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 172; DB 24; Length 417;
Pred. No. 0.00e+00;
0; Mismatches 108; Indels
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National Institute of Agrobiological Resources
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/clone_lib="Rice callus"
76 c 108 g 118
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Rice cDNA from callus
Unpublished (1994)
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Local Similarity 73.18;
es 304; Conservative
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Fax: 0298-38-7468
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A1176862 676 bp mRNA EST 20-JAN-1999
EST220465 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVBX80 3' end, mRNA sequence.
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                                                    1039 GITGTAGAAGAAIGTGGGGAGAACAITTCCAAAGAGCAGITGAAAGACIAIGITIGGAAA 1098
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299 GTAATAGGTGAGACAGGTAGTGATGTTACAACTGATCAACTCAAAGAGTATGTGTGGAAG 358
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                          1099 ACATTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGGAGTTCTGCGAAAGAC 1154
                                                                                                              359 ACACTAAAAAGTGGAAAGGTTGTTCCTGGCTC-GGTCATGGAGTTCTACGTAAGAC 413
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/clone="ROVBX80"
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
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Dept Plant Breeding
Cornell University
Ithaca, Nr 14853-1901, USA
Tel: 607 255 6683
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AA231705
g1854091
AA231705.1 GI:1854091
                                       Query Match 8.1%;
Best Local Similarity 66.7%;
Matches 396; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'-CGGTCGACCGTCGTTTTTTTTTTTT-3'. CDNAs were cloned into the Notl/Sall sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (large:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: embryo; Vector: pSPORT; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: Sal1(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTT" . cDNAs were
                                                                                                                                                                                                                                                                                                                                                                                                                                          AA606966 657 bp mRNA EST 30-SEP-1997 wm94409.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:1005953 5' similar to SW.CISY_PIG PO0889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLN: ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:570169
                                                                                                  1146 CAGAACTCCATGTCCAAAACCAGGGACAACCTTGCCACTGTTCAATGTTTTCCAAACATA 1087
423 TAGGACTGCATGACCATATCCTGGGACAACCCGTCCCGAGTTGAGTGTGTTTCCAGATGTA 482
                                                                                                                                                           601
                                                                                                                                                                                                 1027 ATAGCAAAACTTCCTGATTGGCTAAACCATGAAGTGGTCCGGCTAAACCATTCAAAGCAG 968
                                                                                                                                                                                                                                                                              967 CAGCAAAGGAGGAGATCAGATCAGACAAAGCACTAGCAACCAAGTGACCGGTGTGAGCAC 908
                                                                                                                                                                                                                                       542 AGACAAGCACCTCCTGGTTTGCTAGTCCATGCAGGGCCCTGCCAGCCCATTCATAGCTG
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On Sep 12, 1996 this sequence version replaced gi:1328460
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Ab xref="taxon:10090"

/clone="IMAGE:1005953"

/clone=lib="Knowles Solter mouse blastocyst B1"

/tissue_type="blastocyst"

/dev_stage="embryo (pre-implantation)"

/lab.het="DH10B"

/for 181 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
1. .657
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Poales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  976 AAIGGIITAGCCGGACCACIICAIGGIITAGCCAAICAGGAAGIIIIGGIAIGGAIAAA 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1095 GAAAACATTGAACAGTGGCAAGGTTGTCCCTGGTTTTGGACATGGAGTTCTGCGAAAGAC 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 GAACACACTCAATTCAGGACGGGTGGTCCCAGGATACGGTCATGCAGTACTGAGGAAGAC 318
                                                                                                                                                                                                     141 AATGGGCTGGCGGGCT-CTACATGGACTAGCAAATCAGGAGGTGCTTGTCTGGCTGACA 199
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                                                                                                                                                                                                                                                                                                                82 ACAAGCCATTTGGTGGCCAGCGCATT-TCAGACCCTTACCTGTCCTTTGCAGCAGCAGGTG 140
                                                                                                                                                                                                                                                                                                                                                                                      916 ACCGGTCACTTGGTTGCTTTGTCTTGATCCTTACCTCTCTTTGCTGCTGCTTTG 975
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VanDeynze, A.E., Sorrells, M.E., Park, W.D., Ayres, N.M., Fu, H., Cartinhour, S.W. and McCouch, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA231705 307 bp mRNA EST 27-FEB-199
CD0534.R cDNA from oat Avena sativa cDNA clone CD0534, mRNA
                                                                                                                                                            22 CTCATGCGTTTGTACCTCACCATCCATAGTGACCATGAGGGTGGTAATGTAAGTGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 -CAGCTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTTACGAGACTACATCTG
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Unpublished (1997)
    Length 657;
Score 153; DB 15; Length 65
Pred. No. 3.25e-287;
0; Mismatches 189; Indels
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On Apr 14, 1993 this sequence version replaced gi:693674
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                                                                                                                               /cultivar-_Brooks / Anote-Vector: Unl-ZAP XR/pBluescript; Site_1: EcoRI; Site_2: NhOI: A Uni-ZAP XR CDNA library was constructed from eisolated leaf mRNA from the oat cultivar 'Brooks' and converted to pBluescript (amp resistant) as described in Heun et al. (1991) Genome 34:47-447. Por insert amplification, use M13 forward and reverse primers. Clones from this library are designated with the prefix CDO'. *Note: Clone CDO1081 was recloned into the TA //db_xref="taxon:4498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          967 GCTGCTTTGAATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTA 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1027 TGGATAAAATCTGTTGTAGAAGAATGTGGGGAGAACATTTCCAAAGAGCAGTTGAAAGAC 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TACGTATGGAAGACACTGAAGAGTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CGTAATACAGATCCACGATACTCGTGCCAAAGGGAGTTTGCACTTAAGTATTTACCCGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GACCCACTTTTCCAACTGGTCTCCAAGTTGTACGAAGTTGTGCCTCCTATCCTTACTGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 75; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCGGCACTGAACGGTTTAGCTGGGCCACTGCATGGCCTGGCTAATCAGGAAGTGTTGCTA 60
                     CDO534. Sequence determined by Nicola M. Ayres. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 307;
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Pred. No. 5.79e-280;
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                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="cDNA from oat"
                                                                                                                 /organism="Avena sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 g
                                                                                                                                                                                                                                                                                                                                                                                           /clone="CD0534"
Email: srm4@cornell.edu
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Best Local Similarity 75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
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/strain="var columbia" /strain="var columbia" /strain="var columbia" /strain="var columbia" /note="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not: Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were l) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primad cDNA. "Ab vref="raxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS AA313713 501 bp mRNA EST 19-APR-1997 DEFINITION EST185581 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to citrate synthase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GTCGAAAGACTTGGCGAACCGTGCTGC-TGTGCCAGATTATG-TGTACAATGCCATCGAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 GCTCTGCCTTCCACAGCTCATCCAATGACTCAATTTGCTAGCGGTGTTATGGCCCTCCAG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 GTGCAAAGTGAGTTTCAAAAGGCATATGAGAATGGAATTCATAAGTCAAAGTTCTGGGAG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 CCAACATATGAGGATTGCCTCAACCTGATTTGCTCGTGTTNCCTGTTGTAGNCTGCATAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 CCAACATATGAGGATTCCATGAATCTGATT-GCTCAAGTT-CCACTTGTTG-CTGCTTA- 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 ICITIAICCGAAGGGAIGIAIAANAAIIGGIGGIICCAIICCCICAGGAIAAAACCIIIG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCTTTTGTGGGCTTCTCTTAACTGGAAAGGTACCTAGCAAAGAGAGCAAGTTGAAGCACT- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 ATACCTGAATGCCAAAAGGTATTACCTGCAGCAAAGCCTGGGGGTGAGCCCTTGCCTGAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 GGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAATT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ATTCCTGAGTGCCAGAAAGTATTACCTACTGCCCCAGTCTGGAGCTGAACCATTACCGGAG 62
                                                                                              MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.79e-280;
0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                    /organism-"Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="873F09; 1q21.3-1q23.2; 9"
/clone="189H3T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 150; DB 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 t
                               MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Lambda-PRL2"
106 c 122 q 14
                                                                                                                                               Tel: 517-353-vec.
Fax: 517-353-9168
Enail: 22313tcneibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 g
                                                       Michigan State University
Contact: Thomas Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 GNTINIGGGNNNAAATTI 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.9%;
Best Local Similarity 73.3%;
Matches 321; Conservative
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US-08-702-718-1.rst

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1 (Dases to 501)

S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, K.G., Goorane, J.D.,
Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, Man Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhuad, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nayen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
L. Kunsch, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,
Raymond, L., Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           963 TGCTGCTGCTTTGAATGGTTTAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTT 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1023 GCTATGGATAAAATCTGTTGTAGAAGAATGTGGGGGAGA-ACATTTCCAAAGAGCAGTTGA 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: Mon!
/db_xref="ArCC (inhost):109839"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TGTCTGGCTAACA-CAGCTGCAGAAGGAAGTTGGCAAAGATGTGTCAGATGAGAAGTTAC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGCAGCAGCCATGAACGGGCTGGCAGGGCCTCTCCATGGACTGGCAAATCAGGAAGTGCT 60
                                                                                                                                                                                 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 144; DB 11; Length 501;
Pred. No. 1.68e-265;
0; Mismatches 153; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Apr 14, 1993 this sequence version replaced gi:693326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Colon carcinoma (HCC) cell line'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="colon"
/cell_type="KM12C"
/cell_line="KM12C(HCC)-parental human colon
carcinoma;Dukes B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
                                                         AA313713.1 GI:1966042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_ESTs: THC171646
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Best Local Similarity 67.4%;
Matches 327; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bioinformatics
                                                                                                                                                       Homo sapiens
                            q1966042
                                                                                                                          human
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                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
ACCESSION
                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                           AUTHORS
                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                         VERSION
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7773 vector. Library constructed and normalized by Bento Scares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS AA237580 522 bp mRNA EST 03-MAR-1997
DEFINITION mxlld01.rl Soares mouse NML Mus musculus cDNA clone IMAGE:679873 5'
similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL
PRECURSOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Mylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
1082 AAGACTATGTTTGGAAAACATTGAACAGGGGAGGTTGTCCCCTGGTTTTGGACATGGAG 1141
                                                                                          1202 CTGAAGATCCACTGTTTCAACTGGTTTCAAAACTCTACGAAGTTTTCCTCC-TGTTCTTA 1260
                                                                                                                                                                                                                                                                                                                        1319 TGAACTATTATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGCGTATCAAGAG 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 TAGAGCAGGGTAAAGCCAAGAATCCTTGGCCCAATGTAGATGCTCACAGTGGGGTGCTGC 359
                                                                                                                                                                                                                                                                                                                                                                                                          360 TCCAGTATTATGGCATGACGGAGATGAATTACTACACGGTCCTGTTTGGGGTGTCACGAG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 CATIGGGIGTACTGGCACAGCICATCTGGAGCCGAGCCTTAGGGITCCCTCTAGAAAGGC 479
                                                         180 TACTAAGGAAGACTGATCCGCGATATACCTGTCAGCGAGAGTTTGCTCTGAAACACCTGC 239
                                                                                                                                                                         240 CTAATGACCCCATGTTTAAGTTGGTTGCTCAGCTGTACAAGATTGTGCCCAATGTCCTCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1392879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 453.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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JOURNAL
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SOURCE
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DEFINITION ATTS0029 AC16H ARAbidopsis thaliana cDNA clone TAT2B1 5' similar to
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR Swiss-Prot entry POGR89,
mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1189 ATGAAGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTTCAAAACTCTACGAAGTTTTC 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1249 CTCC-TGTTCTTACAGAACTTGGCAAAGTTAA-AACC-TTGGCCAAATGTTGATGCCCAC 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1010 ATCAGGAAGTTTTGCTATGGATAAAATCTGTTGTAGAAGAATGTGGGGGAGA-ACATTTCC 1066
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                                                                                                                                                                                                                                                                                                                                                                 890 ATGAAGGTGGTAATGTCAGTGCTCACACCGGTCACTTGGTTGCTAGTGCTTTGTCTGATC 949
                                                                                                                                                                                                                                                                                                                                                                                                            59 CTTACCTGTCCTTTGCAGCCATGAATGGGCTGGCGGGCT-CTACATGGACTAGCAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 ATCAGGAGGTGCTTGTCTGGCTGACA-CAGCTACAGAAGGAAGTTGGCAAAGACGTGTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GATGAGAAGTTACGAGACTACATCTGGAACACACTCAATTCAGGACGGGTGGTCCCAGGA 236
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                                                                                                                                                                                                                                                                                                                   1 ATGAGGGTGGTAATGTAAGTGCCCACACAAGCCATTTGGTGGG-AGCGCTGT-TCAGACC 58
                                                                                                                                                                                                                         Score 136; DB 10; Length 522;
Pred. No. 2.69e-246;
0; Mismatches 165; Indels 8; Gaps
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                                                                                    /clone_lib="Soares mouse NML"
/tissue_type="Liver"
                                                                                                                                                          118 t
                /db_xref="taxon:10090"
/map="3"
                                                              /clone="IMAGE:679873"
                                                                                                                                                          150 9
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125 c 150
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Arabidopsis thaliana
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Local Similarity 66.9%;
les 349; Conservative
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I., Lescure B. UMR05 CNRS/INRA

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/note-Tvector: Lambda ZAPII; tissue-cell suspension culture of ecotype columbia; clone_library-AC16H; Cloning vector: Lambda ZAPII; Physiological condition: cycling cells."
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Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 2292 Std Error: 0.00

Seg primer: -28M13 rev2 from Amersham

High quality sequence stop: 423.

I.o.466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 AGTGCACTTTCAGACCCATATCTGTCATTTGCAGCTGCATTAAATGGTTTAGCTGGGCCA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 CICCAIGGIIIGGCIAAICAGGAAGIIIIGGCIIIGGAICAA-ICAGICGIAGAGGAAIGI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      874 ACAATACACAGIGAICATGAAGGIGGIAAIGICAGIGCICACACCGGICACITGGIIGCI 933
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(Dases 1 to 466; Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hultman, M., Kucaba, T., Le, M., Lenono, G., Marra, M., Parsons, J., Fifkin, L., Pohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, P. Wabhy Merch EST Project
Unpublished (1993 this sequence version replaced gi:693136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 35; Indels 2; Gaps
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
laboratoire de Biologie Moleculaire
BP 27,31332 Castanet-Tolosan cedex,France
Email: lescuredtoulouse.inra.fr.
Location/Qualifiers
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Local Similarity 82.3%; Pred. No. 4.57e-220;
es 172; Conservative 0; Mismatcher 22
                                                                                                                                                            /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/clone="TAT2B1"
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Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                MSU-LOCALIDATION MAINTENANCE OF THE STANDARY MAINTENANCE OF TAXABLE OF THE SEG Primer: To due primer.

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Location/Qualifiers

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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from large scale partial sequencing of anonymous Arabidopsis cDNA clones plant physiol. 106, 1241-1255 (1994)
On Sep 12, 1996 this sequence version replaced gi:1405145.
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             916 ACCGGTCACTTGGTTAGTTGTTGTCTGATCC-TTACCTCTCTTTGCTGCTTTT 974
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Pred. No. 3.23e-208;
0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                             1 others
                                                                                                                                                                                                                                                                                     /lab_host-"SOLR (kanamycin resistant)"
116 c 122 g 110 t 1 oth
                                                                                                                                                                                                                          /clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
                                                                                                                                                                                                         /clone-"IMAGE:562451"
                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                          122 g
                                                                                                                                                                                                                                                                   /dev_stage="adult"
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Best Local Similarity 69.3%;
Matches 259; Conservative
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/organism="Arabidopsis thaliana"
/strain="var columbia"
/strain="var columbia"
/strain="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1)
quantities of 4 pools of mRNA. The mRNA sources were 1)
quy germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
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Wan,C.-H., Yu.Y., Sasinowski,M. and Wing,R.A.
Cotton EST Database: Sequence Analysis of 2000 cDNA Clones from an
Abscission Zone Library
Unpublished (1998)
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Malvales; Malvaceae; Gossypium.
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Best Local Similarity 79.5%; Pred. No. 2.02e-196;
Matches 159; Conservative 0; Mismatches 39;
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Clemson University Genomics Institute
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Score 116; DB 22; Length 585;
Pred. No. 8.91e-199;
0; Mismatches 90; Indels 15; Gaps 13;
                                                                                                                                         /organism="Gossypium hirsutum" / note="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI; This is a Uni-ZAP XR custom cDNA library made by Stratagene (U.S.A.: 1-800-424-5444): Stratagene cat.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: SP030 (AACAGCTATGACTATA)
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                                                                                             High quality sequence stop: 239.
Location/Qualifiers
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Best Local Similarity 73.7%;
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Search completed: Sat Oct 23 16:24:08 1999 Job time : 3223 secs.

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	(AE)
Releas Copyri	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Run on:	Sat Oct 23 17:41:52 1999; MasPar time 2810.72 Seconds
Tabular output n	not generated.
Title: Description: Perfect Score:	>US-08-702-718-3 (1-1551) from US08702718.seq
N.A. Sequence: Comp:	1 TCCTCTAACCTTGACCTTCGAAAAAAAAAAAAAA
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	646147 segs, 1385953633 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	<pre>embl58 l:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_huml 6:em_hum2 7:em_in 8:em_om 9:em_cr 10:em_ov 11:em_pat 12:em_ph 13:em_pl 14:em ro 15:em sts 16:em v1</pre>
Database:	genbank111 17:9b_ba1 18:9b_ba2 19:9b_htg1 20:9b_htg2 21:9b_in1 22:9b_in2 23:9b_om 24:9b_ov 25:9b_pat 26:9b_ph 27:9b_p11 28:9b_p12 29:9b_pr1 30:9b_pr2 31:9b_pr3 32:9b_rc 33:9b_st 34:9b_sts 35:9b_sy 36:9b_un 37:9b_vi
Statistics:	Mean 11.735; Variance 9.742; scale 1.205

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	5.28e-285	1.94e - 263	1.75e-137	5.60e-137	2.56e-85	
	Description	Sequence 2 from Patent	B. vulgaris mRNA for ci	Citrus maxima citrate	Sequence 3 from Patent	N. tabacum mRNA for cit	Daucus carota mRNA for	S.tuberosum mRNA for m	Sequence 1 from Patent	Arabidopsis thaliana m	Populus hybrid mRNA fo	Homo sapiens citrate s	Porcine citrate syntha	S.cerevisiae mitochond	
	DI	A46546	BVCITSYNH	CMU19481	A46547	NTCITSYNH	AB017159	STCITS	A46545	ATMTCITRN	PHCITSYNH	AF047042	PIGCITSYN	SCMTCISNA	
	Query Match Length DB	1551 25	1551 27	1733 27	1747 25	1747 27	1859 27	1891 27	1891 25	1680 27	1378 27	1401 31	1455 23	1481 27	
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	Score	1551	1551	741	726	726	721	664	664	608	266	319	318	215	
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Yeast gene for citrate 2.56e-85 S.cerevisiae chromosom 2.56e-85 S.pombe chromosome 2.56e-85 S.pombe chromosome 1 C 6.46e-75 Yeast (S.cerevisiae) C 5.70e-71 Yeast (S.cerevisiae) C 5.70e-71 S.cerevisiae chromosom 5.70e-71 S.cerevisiae chromosom 5.70e-71 S.cerevisiae chromosom 5.70e-71 Candida tropicalis DNA 4.33e-64 Aspergilus niger mRNA 3.93e-35 Kluyveromyces lactis D 5.81e-30 N.crasa mitochondria D.72e-20 Caenorhabditis elegans 9.58e-21 human STS WI-12459. 2.18e-19 Arabidopsis thaliana C 3.81e-17 T. thermophila mRNA fo 1.06e-16 Caenorhabditis elegans 8.20e-16 Emericella nidulans ci 2.61e-12 S.cerevisiae chromosom 7.06e-12 S.cerevi	444000000	PAT 07-MAR-1997 4487. reptophyta; Embryophyta; Tracheophyta;	eae; Beta. .U. LOWER FORMATI	28 25 14. 026"	is in conflict with the conceptual SE"
SCCSO1 SCINROOLC SCANROOLC SCANCOLL952 SCCIT2 SCCIT2 SCCIT2 ABOOLISE ABOOLI		DNA int W0952 int W0952	yllaly schue: 3 AND 14-SE GMBH 38821	35366 96 67995 95 08629 95 fiers a vulgar LINIE 58 n:3555 LEAF*	/note="Protein sequence : translation." /codon_start=1 /product="CITRATE SYNTHAX /protein_id="CAA02909.1" /db_xref="PlD:e306423"
е н н	1797 2 10772 2 1329 2 1436 2 2286 2 11892 2 15892 2 15802 3	10 C T	— m 2. ↔ ti o	r publication DE 44, r publication AU 20, r publication DE 44, Location/Quali, 1.1518. / Organism-"Bet, / Strain-"ZUCHT, / Ab_xref-"taxoo/ / Lissue_type-", / Clone-"PSBCS" / Lissue_1333 / EC_number-"4.	/note="Pr translati /codon_st /product= /protein_ /db_xref=
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La cognata, U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B. (bases 1 to 1551)

La Cognata, U.
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euphyllophytes: Spermatophyta: Magnollophyta: eudicotyledons:
Caryophyllidae: Caryophyllales; Chenopodiaceae: Beta.

    (bases 1 to 1551)

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Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
841 CTGCTGTGGATTAAAICAGTTGTTGATGAATGTGGAGAGAACATCTCGACAGAGCAGTTG
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DSPQMLELMRLYVTIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLA
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FALKHLEDDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTBARYY
TULFGVSFIJTGSQLIMPLEPPKSVTWEWLEKFCKFRA"
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                                       /translation-"SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGG
MRGMTGLLWETSLLDPEEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVP
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/db_xref="PID:92300710"
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/translation="SSNLDLRSELQELIPEQGERLKKIKKEFGSFOLGNINVDMVLGG
MRGMTGLIMETSLIDPEGGIRRAGST PEGGKLLTBAAGAGBELPEGLTMLLLTGKVP
SKEGVPDALSADLGKRAGIPDHVYKTIDALPITAHPWTGCFGVMALQTRSEFGKAYEK
GIHKSKFWEPTYEDCLSLIAQVPVVAAVYTRMYKNGQVIPLDDSLDYGGNRAHLGF
SPGMLEJMKLYVI HSDHEGGNVSAHTGHLVGSPLSDPSLSFAAALNGLAGPLHGLA
NOEVLLMIKSVVDEGGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTGGRE
FALKHLPDDPFFQLVSKLYEVVPPILLELGKVKNPWPWVDAHGGVLNHYGLTEARYY
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                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="citrate (si)-synthase"
/protein_id="cAA5910.1"
/db_xref="PID:e137433"
/db_xref="PID:g1556380"
/db_xref="G1:1556380"
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
'db_xref="taxon:3555"
....1314
                                                                               /EC_number-"4.1.3.7"
                                                                                              /codon_start=1
                             /gene="cit1"
                                              <ī. .1314
/gene="cit1"
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 1551; Conservative
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Citrus maxima citrate synthase (cit) mRNA, nuclear gene encoding mitochondrial protein, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIGAACCACTAIGGIIIGACAGAAGCAAGAIACIAIACGGIIIIGIIIGGGGIATCAAGG 1200
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                                                                                                                                ITTGCAGCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTC 840
721 AATGITAGIGCACACIGGCCAITIGGIGGGIAGICCACTIICAGAICCITATIIGICA 780
                                                                                                                                                                                                                                                                                                                                                                                                                841 CTGCTGTGGATTAAATCAGTTGTTGATGAATGTGGAGAGAACATCTCGACAGAGCAGTTG 900
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Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Magnollopsida; Rutanae; Sapindales; Rutaceae; Citrus.
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Canel, C., Bailey-Serres, J. and Roose, M. Physiological and molecular genetic studies of acid accumulation in
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VAAYVYQRIYKDGKIIPKDDSLDYGGNFSHMLGFDDPKMLELMRLYVTIHSDHEGGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAHTGHLVASALSDPYLSFLAALNGLAGPLHGLANQEVLLWIKSYVDECCENTTEQL
SYVWATLANGGKVVPGFGHGVLRKTDBRYTCQREFALKHLPDDPLFQLVSKLYEVVPP
ILTKLGKVKNEWPNDAHSGVLLNHFGLAEARYYTVLFGVSRSLGICSQLIWDRALGL
PLERPKSVILDWIEKNCKKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSIPECQKLLPAAKPDGEPLPEGLLWLLLTGKVPSKEQVDGLSKELRDRATVPDYVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MASLRSATALSRLRSRAGQQSNLSNSVRWLQMQSSADLDLHSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEMIPEQQERLKKVKSDLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDPDEGIRFRG
                                                                                                Thesis (1994) Botany & Plant Sciences, University of California at
                                                                                                                                                                                                                  Submitted (04-JAN-1995) Camilo Canel, University of California at Riverside, Botany & Plant Sciences, Riverside, CA 92521-0124, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                            /strain="Siamese sweet (pummelo 2240)"
//ostain="There is a single copy of the cit gene in the citrus genome. A single transcript with an estimated length of 1,850 nucleotides can be detected in juice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="synthesis of citrate from oxaloacetate and acetylCoA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 CTGATCTTGACCTTCATTCTCAGGTCAGGAAATGATTCCAGAACAACAGGGGGCGCTGA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 TTGGCGGGATGAGAGGAATGACTGGCTTACTTTGGGAAACCTCATTACTTGACCCTGATG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="synthesis of citrate from oxaloacetate and acetylcoA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 AGAAGATAAAGAATTTGGAAGTTTCCAGCTGGGGAATATCAATGTTGACATGGTAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CTAACCTTGACCTTCGTTCAGAGTTACAAGAACTGATTCCTGAACAACAGGAACGACTGA 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="targets the protein to the mitochondrial
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Pred. No. 0.00e+00;
0; Mismatches 287; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="citrate synthase precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="juice cell"
/tissue_type="juice tissue"
/dev_stage="immature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 t
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                                                                                                                                                                                                                                                                                                                        /organism="Citrus maxima"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA82743.1"
/db_xref="PID:g624676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:37334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="hermaphrodite"
                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                            2 (bases 1 to 1733)
Canel, C.
Direct Submission
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57 1472
1 (bases 1 to 1733)
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1710. .1716
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Best Local Similarity 78.2%;
Matches 1028; Conservative
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943 IGGCCGCATTAAATGGTTIAGCTGGACCACTCCATGGTTTGGCTAATCAGGAAGTTTTGC 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1085 AGCTIGGAAAGGIAAAGAATCCAIGGCCIAAIGIIGAIGCICAIAGIGGAGTIIIGCIGA 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1303 ACCATTTTGGTTTGGCTGAGGCAAGATATTATACTGTTCTTTTTGGAGTATCAAGGAGTC 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1363 TTGGGATCTGCTCTCAGTTGATATGGGACCGAGCTCTTGGGCTGCCACTTGAGAGGCCAA 1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 ATTATGTGTACAAGGCCATTGATGCTCTACCTGTATCGGCACATCCGATGACTCAGTTTG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 CTAGTGGGGTCATGGCTCTGCAGGTGCAAAGTGAATTTCAGGAGGCTTATGAGAAGGGAA 642
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                                                                                           343 AGGGAATTCGCTTTCGGGGTCTGTCTATTCCTGAGTGCCAGAAGTTGTTACCTGCCGCTA 402
                                                                                                                                                           185 AGGGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCTGCAA 244
                                                                                                                                                                                                                           403 AGCCAGATGGAGAACCTTTGCCTGAGGGTCTTCTTTGGCTTCTTTAACTGGAAAGGTAC 462
                                                                                                                                                                                                                                                                                 245 GIGCIGCIGCAGAGCCAIIGCCIGAAGGICIICITIIGGCIICITIIAACCGGAAAGGIIC 304
                                                                                                                                                                                                                                                                                                                                                       463 CGAGCAAAGAGCAGGTCGATGGCTTGTCCAAGGAATTGAGAGATCGTGCCACTGTCCCAG 522
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                              125 TGGGCGGAATGAGAGGAATGACTGGTTTAGTTTTGGGAGACTTGGTTAGTGGACGAGAAG 184
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LSIYECQKVLPAAKPGGEPLPEGLLMLLLTGKVPSKEQVDSLSQELRSRATVPDHVYK
TIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPIYEDSMSLIAQVPL
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SAHTOHLVARALSDPYLSFAAALNGLANGYLLMYKRVYEGCENISKEQL
KDYAMKTLKSGKVYGGFGHGVLKKUDPRYTCQREFANGYKLLKHLPEDPLFGLYAKTYETVEL
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                                                                                                                                                                                                                                                                              Nicotiana tabacum
Wararyota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
I (bases I to 1747)
Mueller-Roeber B., Landschuetze, V. and La, C. U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
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1205 TIGGAATAIGCTCACAGCTTATAIGGGACCGAGCTCTIGGCTIGCCGCTAGAGAGGCCCAA 1264
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                                  1423 AAAGTGTAACTTTAGATTGGATTGAGAAAATTGGAAGAAAGCAGCTTAGAATTG 1477
                                                                       1265 AGAGTGTCACTATGGAATGGCTTGAAAAGTTTTGTAAAAGAAGAGCATAACATTG 1319
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Pred. No. 0.00e+00;
0; Mismatches 277; Indels 3;
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/organism="Nicotiana tabacum"
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/db_xref="PID:e306253"
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HOECHST SCHERING AGREVO GMBH (DE)
Other publication DE 4438821 960425
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Sequence 3 from Patent W09524487.
A46547
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/clone="TCS"
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/EC_number="4.1.3.7"
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Matches 1021; Conservative
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1081 TTAGAGCTTGGAAAGGTAAAGAATCCATGCCTAATGTTGATGCTCATAGTGGAGTTTTG 1140
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181 GAAGAGGGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCT 240
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                                                                                    412 GCAAAGCCTGGGGGAGAGCCCTTGCCTGAAGGTCTTGTCTGGCTTCTTTTAACAGGAAAG 471
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/translation-"MVFYRGVSLLSKLRSRAVQGTNLSNSVRMLQVQTSSGLDLRSEL
GELPEQQDREKKLKSHFKVQLGNTYDDWLGGRRGMTGLAFETSLDPDEGTRFRG
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TIDALPVTAHPMTGFATGVMALQVQSEFQRAFEKGIHKSKLWEPTYEDSMSLIAQVPL
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SAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANDEVLLWTKSVVEECGENISKEQL
SVAWWTLKSCKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQ
FLQNLAKLINPWNUAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP
LERPKGYTMEWLENKKA"
335 C 400 9 522 t
                                                                                                                                                                                                                                                                                     1 (bases 1 to 1747)
La Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B.
2 (bases 1 to 1747)
La Cognata,U.
La Cognata,U.
La Cognata,U.
                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Nicotlana.
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                                07-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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/protein_id="CAA59008.1"
/db_xref="PID:e137432"
                           NTCITSYNH 1747 bp mRNA N. tabacum mRNA for citrate synthase.
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/db_xref="G1:1556429"
/db_xref="SPTREMBL:024135"
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                                                                                                                                                  citl gene; citrate synthase, common tobacco.
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70 1470
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Best Local Similarity 78.5%;
Matches 1021; Conservative
                                                                                                                           GI:1556428
                                                                                                                                                                                                  Nicotiana tabacum
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241 GCAAGTGCTGGTGCAGAGCCATTGCCTGAAGGTCTTGTTTTGGCTTTTTTAAGCGGAAAA 300
                                                                                            301 GTTCCTAGGAAAGAGCAAGTAGATGCTCTATCAGGAGATTTACGAAAACGTGCTTCTATC 360
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GLSIPECQKLLPGAKPGGEPLPEGLLWLLLTGKVPTKEQVDALSAELPSPAAVPEHVY
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                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eughyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Araliales; Aplaceae; Daucus.

(Dases 1 to 1859)

Takita, E., Koyama, H., Shirano, Y., Shibata, D. and Hara, T.
Direct Submission
Submitted (26-AUG-1998) to the DDBJ/EMBL/GenBank databases. Eiji
Takita, Gifu University, Laboratory of Plant Cell Technology,
Faculty of Agriculture; Yanagido 1-1, Gifu, Gifu 501-1193, Japan
(E-mail:takitaecc.gifu-u.ac.jp, Tel:+81-58-293-2911,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                           Daucus carota (cultivar:MS Yonsun) suspension cultured cells CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takita,E., Koyama,H., Shirano,Y., Shibata,D. and Hara,T. cDNA encoding carrot mitochondrial citrate synthase Published Only in DataBase (1998) In press Location/Qualifiers
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      carota mRNA for citrate synthase, complete cds
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1. .156
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Pred. No. 0.00e+00;
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/protein_id="BAA32557.1"
/db_xref="PID:d1033521"
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/db_xref="taxon:4039"
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/gene="DcCS"
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Best Local Similarity 78.0%;
Matches 1005; Conservative
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Takita, E., Koyama, H.
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AAGCCCGGTGGAGAACCATTGCCTGAGGGTCTGCTCTGGCTTCTTTTAACTGGAAAGGTA 564
                                                                           244 AGIGCIGGIGCAGAGCCAIIGCCIGAAGGICIICIIIGGCIICIIIIAACCGGAAAGGII 303
                                                                                                                                                               CCAACTAAAGAGCAAGTAGATGCATTGTCCGCAGAGTTGCGAAGTCGTGCTGCTGTACCA 624
                                                                                                                                                                                                                                               304 CCTAGCAAAGAGCAAGTAGATGCTCTATCAGCAGATTTACGAAAACGTGCTTCTATCCCA 363
                                                                                                                                                                                                                                                                                                                                   625 GAGCATGTATACAAAACCATCGATGCGTTACCTGTTACAGCTCATGCAATGACTCAATTT 684
                                                                                                                                                                                                                                                                                                                                                                                                                   364 GACCATGTGTACAAAAAATGATGCTCTACCTATTACGGCTCATCCAATGACTCAGTTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 GCAACTGGTGTCATGGCCCTCCAGGTTCAAAGTGAATTTCAGAAGGCATACGAGAAAGGG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 ATTCACAAAACAAAGTATTGGGAGCCAACATATGAGGACTCTATTACTTTAATTGCTCAA 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               925 AGCATGCAAGAGCTTATGAGGCTTTACGTTATCCATACTGACCATGAAGGTGGAAAC
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LLFLQNLAKLKFWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG
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Planta 196 (4), 756-764 (1995)
                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes: Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
                                                                                                                                                                                                                                                    Landschuetze,V.
Direct Submission
Submitted (20-SEP-1993) V. Landschuetze, Inst. fuer Genbiologische
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Pred. No. 0.00e+00;
0; Mismatches 261; Indels 12;
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Landschutze, V., Muller-Rober, B. and Willmitzer, L.
                               S.tuberosum mRNA for mitochondrial citrate-synthase.
X75082
9483509
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1264 AAGAGTGTCACTATGGAATGGCTTGAAAA 1292
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mitochondrial citrate synthase
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443 AAGGTCTTCTCTTCTTTTAACAGGAAAGGTGCCATCAAAAGAGCAAGTGAATTCAA 502
                                                                                                                                                                               269 AAGGTCTTCTTTGGCTTCTTTTAACCGGAAAGGTTCCTAGCAAAGAGCAAGTAGATGCTC 328
                                                                                                                                                                                                                                                             TTGTCTCAGGAATTGCAGAGTCGGGCATCATATCCCTGATCATCATGTATACAACTATTG 562
                                                                                                                                                                                                                                                                                                                                   TAICAGCAG-ATITACGAAAACGIGCTIC-TAICCCAGACCAIG-IGIACAAAACAATIG 385
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LLFLQNLAKLKPWPNYDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG
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Mueller-Roeber, B., Landschuetze, V. and La, C.U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
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DCRLPECQKALLPTAQSGGLNHYRRSFVASLNWKGTLAKSKLKHCRKTWNRAAVSDYV
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PVVAAVYYRRWYKNGDSIPSDKSLDYGANFSHHLGFDDERLKELMRLTSPSTVWHEGG
NVSAHTGHLVGSALSDPYLSFAAALUNGLAGPLHGLANQEVLLMIKSVVEEGGEDISKE
QLKEYWKTLIANGGYLPGYGHOYLRNTDPRYVCQREFALKHHPDDPLFQCCKLMKLAS
CLIELESEEPWPNVDAHSGVLLNHYGLIEBRYYTVLFGVSRLGICSQLIWDRELLLA
                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnollophyta; eudicotyledons; Rosidae, Capparales, Brassicaceae, Arabidopsis.
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Unger, E.A., Hand, J.M., Cashmore, A.R. and Vasconcelos, A.C.

Isolation of a CDNA encoding mitochondrial citrate synthase from

Arabidopsis thaliam Plant Mol. Biol. 13 (4), 411-418 (1989)
                            Arabidopsis thaliana mRNA for mitochondrial citrate synthetase, X17528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 GCGGAATGAGAGGAATGACTGGTTTACTTTGGGAGACTTCCTTACTCGACCAGAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 608; DB 27; Length 1680; Pred. No. 5.28e-285;
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="citrate synthetase"
/protein_id="CAA35570.1"
/db_xref="PID:e1188578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref-"SWISS-PROT:P20115"
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/db_xref-"GI:2652924"
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345 c 408 g 4
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/EC_number="4.1.3.7"
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                    1680 bp
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Similarity 77.6%;
                                                                                                                                                    Arabidopsis thaliana
                                                                                            GI:11243
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thale cress.
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                                                                                                                                                                                                                                                AUTHORS
TITLE
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KEYWORDS
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945 ATTTGCAGCTGCATTAAATGGTTTAGCTGGGCCACTCCATGGTTTGGCTAATCAGGAAGT 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1065 GAAAGAATATGTTTGGAAAACATTAAACAGTGGCAAGGTTATTCCGGGATATGGTCACGG 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1125 IGTICIGCGCAATACIGAICCAAGAIAIGIAIGCCAAAGAGAAIITIGCCIIGAAGCAICA 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       960 AGTATIGCGGAAGACAGATCCAAGATACACATGCCAAAGAGAATITGCGTIGAGCACTT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1185 TCCTGACGACCC-TCTTTTCCAGTGTTG-CAA-GCT-TATGAAGTTG-GCCTCCTGTCTC 1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1080 ATTAGAGCTTGGAAAGGTAAAGAATCCATGGCCTAATGTTGATGCTCATAGTGGAGTTTT 1139
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840 CCTGCTGTGGATTAAATCAGTTGTTGATGAATGTGGAGAGAACATCTCGACAGAGCAGTT 899
                                                                                                          TITGCTAGCGGTGTTATGGCCCTCCAGGTGCAAAGTGAGTTTCAAAAGGCATATGAGAAT 645
                                                                                                                                                                               421 TITIGCACIGGIGITATGGCCTIACAGACICGAAGCGAATITCAGAAGGCATATGAGAAA 480
                                                                                                                                                                                                                                                       646 GGAATICATAAGICAAAGITCIGGGAGCCAACAIAIGAGGAIIGCCICAACCIGAIIGCI 705
                                                                                                                                                                                                                                                                                                                               481 GGGATCCATAAGTCAAAGTTTTGGGAGCCAACATATGAGGACTGCCTTAGTTTGATTGCT 540
                                                                                                                                                                                                                                                                                                                                                                                                       706 CGTGTTCCTGTTGTAGCTGCATATGTTTATCGAAGGATGTATAAGAATGGTGATTCCATT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 CAAGTTCCTGTTGTTGCAGCTTATGTTTATCGGAGGATGTATAAGAATGGACAAGTAATA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766 CCCTCAGATAAAICTIIGGAITAIGGIGCAAAITIIIICCCACAIGIIGGGAITIGAIGAI 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720 AAAIGITAGIGCACACACGGCCATTIGGIGGGIAGICCACTITICAGAICTTATTIGIC 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          826 GAAAGGTTGAAAGAGCTCATGAGGCTT-ACATCACCATCCACAGGGTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           780 ATTIGCAGCAGTAAATGGTTIGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 GAAAGATTATGTTTGGAAGACACTAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGG
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Direct Submission
Submitted (06-FEB-1998) Molecular Cardiology Institute, 75 Raritan
Avenue, Highland Park, NJ 08904, USA
Location/Qualifiers
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                                                                                                                       614 TTAAAGACTATGTTTGGAAAACATTAAATAGCGGAAAGGTTGIICCTGGAIITGGTCAIG 673
                                                                                                                                                                                                                                                                                                                                                                               674 GAGIICIACGCAAAACIGIACCAAGAIATACAIGICAAAGGGAGIIIGCAIIGAAGCAII 733
                                                   719 GAAAIGITAGIGCACACAGGCCAITIGGIGGGTAGICCACITICAGAICCTIAITIGI 778
                                                                                                                                                                                          554 ITCTCCTTTGGAICAAAICCGTGGTAGAAGAGTGTGGAGAGATATAACCACAGAACAAC 613
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1401)
Goldenthal,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning and sequence analysis of human citrate synthase CDNA Unpublished
       434 GGAATGICAGTGCICATACTGGICACCTGGITGCIAGTGCACITICAGATCCTIAICTIT
                                                                                                                                                                                                                       899 IGAAAGAITAIGITIGGAAGACACIAAACAGIGGCAAGGITGIACCIGGAITIGGICIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      794 ITACCCAGCTGGGCAAGGTTAAAAACCCATGGCCTAATGTTGATGCTCACAGTGGGGTGT
                                                                                                 494 CATTIGCAGCISCATIGAATGGTITAGCIGGGCCACICCATGGCTIGGCAAATCAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                             959 GAGTATTGCGGAAGACAGATCCAAGATACACATGCCAAAGAGAATTTGCGTTGAAGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF047042 1401 bp mRNA PRI
Homo sapiens citrate synthase mRNA, complete cds.
AF047042
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/protein_id-"AAC25560.1"
/db_xref="PID:93288815"
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/db_xref="taxon:9606"
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Goldenthal, M.J.
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/db_xref="Splash212"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Violales; Salicaceae; Populus.

1 (bases 1 to 1378)
La Cognata, U., Landschuetze, V, Willmitzer, L. and Mueller-Roeber, B. Plant Cell Physiol. In press
2 (bases 1 to 1378)
La Cognata, U.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AGTITGCAACTGGTGTTATGGCCCTACAGGTTCAGAGTGAATTTCAAAAAGCCTATGAAA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 AAGGGATCCATAAGTCAAAGTTTTGGGAGCCAACAIATGAGGACTGCCTTAGTTTGATTG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 CTCGTGTGCCAATAGTAGCTTCATATATTTATCGAAGGATTTACAAAGATGGGAAAGTTA 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 ITCCTATGAATGACTCTTTGGTTATAGGTGGAAATTTTTCACACATGTTGGGATTTGATA 373
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                                                                                                                                                                                                             Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
                                                                                                                                                                                                                                                                                                                              /organism="Populus balsamifera subsp. trichocarpa X
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Local Similarity 78.5%; Pred. No. 1.94e-263;
es 780; Conservativa
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16. .1035
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/note="hybrid"
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16. .1035
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OARIKTFRQQHGKTVVGQITVDMAYGGMRGAKGLVYETSVLDPDEGIRFRGFSIPECQ
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                                                                                                                                                                                                                         LVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEKLRDYIWN
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                                                                                                                                                                                         NLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 GACCTGATACCTAAGGAGCAGGCCAGAATTAAGACTTTCAGGCAGCAACATGGCAAGACG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 GIGTAIGAAACAICAGITCIIGAICCIGAIGAGGGCAICCGIIIICCGAGGCIIIAGIAIC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 TTATTTTGGCTGCTGGTAACTGGATGTATCCCAACAGAGGAACAGGTATCTTGGCTCTCA 414
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0; Mismatches 448;
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Best Local Similarity 63.5%;
Matches 785; Conservative
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LVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKGKDVSDEKLRDYIWN
TLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNVLLEQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Eutherna; Artiodactýla; Suiformes; Suina; Suidae; Sus. 1 (bases 1 to 1455)
Evans, C.T., Owens, D.D., Sumegi, B., Kispal, G. and Srere, P.A.
Isolation, nucleotide sequence, and expression of a cDNA encoding
955 GTTGGCAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCTGGAACACCACTCAACTCA 1014
                                                                                        1015 GGACGGGTTGTTCCAGGCTATGCCCATGCAGTACTAAGGAAGACTGATCCGCGATATACC 1074
                                                                                                                                                                                                                             991 reccaaagaariirecerrgaagcactieccigaigaccariitiraatiegigica 1050
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                                                                                                                                       931 GGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAAGATACACA
                                                                                                                                                                                      1135 CAGCTGTACAAGATTGTGCCCAATGTCCTCTTAGAGCAGGGTAAAGCCAAGAATCCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="citrate synthase precursor (EC 4.1.3.7)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine citrate synthase mRNA, complete cds M21197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M21197.1 GI:164418
citrate synthase.
Porcine kidney, cDNA to mRNA, clone PCS4.
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Biochemistry 27, 4680-4686 (1988)
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/note="citrate synthase"
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                                                         185 IGGCCAAAICACIGIGGACAIGAIGIAIGGIGGCAIGAGAGGCAIGAAGGGAIIGGIGI 244
                                                                                                                                     245 ATGAAACATCGGTTCTTGATCCTGATGAGGGCATCCGTTTCCGAGGCTACASTATCCCTG 304
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                     5; Gaps
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                   0; Mismatches 410; Indels
Best Local Similarity 64.6%; Pred. No. 5.60e-137;
                   758; Conservative
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/db_xref-"SWISS-PROT:P00890"
/translation-"WSALLSTTSKSFLSRGSTROCONMOKALFALLNARHYSSASEQT
/translation-"WSALLSTTSKSFLSRGSTROCONMOKALFALLNARHYSSASEQT
/translation-"WSALLSTTSKSFLSRGSTROCONMOKALFALLNARHYSSASEQT
IRREPARTIPEDIOPED-PRABESTEPLPEALFWLLLTGEIPTDAQVKALSADLARRSEIP
EHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLL
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/clone="Plasmid pFCS1 (Suissa et al., EMBO J. 3, 1773-1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.

    (bases 1 to 1481)

1114 AAIGTIGAIGCTCATAGIGGAGTITIGCIGAACCACTAIGGTIIGACAGAAGCAAGATAC 1173
                                           1264 TACACAGTCCTGTTCGGGGTATCACGGGCACTGGGTGTATTAGCACAGCTCATCTGGAGC 1323
                                                                      SCWICISNA 1481 bp DNA PLN 17-FEB-1997
S.Cerevisiae mitochondrial citrate synthase gene, complete CDS.
223259
g313749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * (Masa,M., Suda,K. and Schatz,G. Suissa,M., Suda,K. and Schatz,G. Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening method EMBO J. 3 (8), 1773-1781 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental
/product="the processing site has been determined by
direct N-terminal protein sequencing"
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Lindner,P. and Plueckthun,A.
The effect of point mutations in the hinge of yeast citrate
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Submitted (05-JUL-1993) Peter Lindner, Protein Engineering,
Ax-Planck-Institut fuer, Biochemie, Am Klopferspitz 18a,
Martinsried, D-82152, Fed. Rep., Germany
4 (bases 1 to 1481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thesis (1993) Protein Engineering, Max-Planck-Institut fuer
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Protein_id="CAB80781.1"
/db_xref="PID:g313750"
/db_xref="G1:313750"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Saccharomyces cerevisiae"
                                                                                                                                     1324 CGAGCCTTAGGCTTCCCTCTAGAGAGGCCCAAG 1356
                                                                                                                                                                                1234 CGAGCTCTTGGCTTGCCGCTAGAGAGGCCAAAG 1266
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mitochondrial citrate synthase
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3 (bases 1 to 1481)
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EVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIID
RAVGAPIERPKSFSTEKYKELVKKIESKN"
GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDH
EGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEMLFKLREEVKGDY
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Pred. No. 2.56e-85;
0; Mismatches 462; Indels 0;
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/translation="MSAILSTTSKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQT
LKERFAEIIPAKAQEIKKFKKEHGKTVIGEVLLEEQAYGGMRGIKGLVWEGSVLDPEE
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LGKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSD
HEGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGD
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YEVAGGVLTKHGKTKRPWPNDSHSGYLLOYYGLTEASFYTVLFGVARAIGVLPOLII
DANGAPIERPRSFSTEKKKLVKKIESKN"
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1 (bases 1 to 2427)
                                                                                                                                                                                                                                               1084 AGAAAAACTGATCCTCGTTATACGGCTCAACGTGAATTCGCATTGAAACATTTCCCAGAT 1143
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                                              964 IGGCTATITAAAITGAGAAGAAGIGAAAGGGGGACTATICAAAAGAAACAAITGAAAAG 1023
                                                                                                                                                1024 TACTIGIGGGATACTITGAACGCAGGGAGAGTIGTICCTGGTTATGGCCATGCGGTTTTG 1083
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Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening method
EMBO J. 3 (8), 1773-1781 (1984)
787 GCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTG 846
                                                                                                                                                                                           907 TAIGITIGGAAGACACTAAACAGIGGCAAGGITGTACCIGGAITIGGICTAGGAGIATIG 966
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                                                                                               847 IGGATTAAATCAGTIGTIGATGAATGIGGAGAGAACATCTCGACAGAGCAGTIGAAAGAT
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/db_xref="taxon:4932"
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/db_xref="PID:93603"
/db_xref="GI:3603"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1402 TACTTGTGGGATACTTTGAACGCAGGGAGAGTTGTTCCTGGTTATGGCCATGCGGTTTTG 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1222 TCTGCCCATACTACACATTTAGTGGGTTCTGCCTTATCTTGGCCATACTTATCTTTGGCC 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 982 ICCAAGAAGAATATTGGAGCTATACATTTGAAGATTCGTTAGATCTGCTGGGTAAATTA 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .042 CCTGTTATTGCTTCCAAAATTTATCGTAATGTGTTTCAAGGATGGTAAAATTACTTCAACC 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1102 GATCCTAATGCTGACTATGGTAAAATTTGGCCCAACTTTTGGGCTACGAAAACAAGGAT 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGGTTTGAATGGTTTAGCTGGCCCATTACATGGTCGTGCCAATCAAGAAGTTTTAGAA 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  787 GCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTG 846
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                                                                                                                                                                                                                                                                                                                                                          487 CATAAGTCAAAGTTTTGGGAGCCAACATATGAGGACTGCCTTAGTTTGATTGCTCAAGTT 546
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                                                                                                                                                                                                                                                                  187 GGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCTGCAAGT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                   802 ACTGACGCTCAAGTTAAAGCCCTTTCTGCTGATTTAGCTGCCAGATCAGAAATTCCAGAG 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 AGCAAAGAGCAAGTAGATGCTCTATCAGCAGATTTACGAAAACGTGCTTCTATCCCAGAC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           862 CACGTIATCCAACTITTAGAIAGCCTCCCAAAAGAICTACATCCAATGGCGCAATTTTCT 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 CATGTGTACAAAACAATTGATGCTCTACCTATTACGGCTCATCCAATGACTCAGTTTTGC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            922 ATTGCCGTGACTGCTTTAGAAAGCGAGTCTAAGTTTGCCAAAGCATATGCTCAAGGTGTA 981
                                                                                        622 GGTGGTATGAGAGGTATTAAAGGCCTTGTTTGGAAGGTTCCGTGTTAGACCCCGGAAGA 681
                                                                                                                                             127 GGCGGAATGAGAGGAATGACTGGTTTACTTTGGGAGACTTCCTTACTCGACCCAGAGAG 186
                                                                                                                                                                                                         682 GCTATTAGATTTAGGGGTCGTACTATTCCAGAAATTCAAAGGGAACTACCAAAGGCTGAG 741
                               Gaps
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Best Local Similarity 59.4%; Pred. No. 2.56e-85; Matches 677; Conservative 0; Mismatches 462;
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GKLPVTASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLLIHSDH
EGGNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDY
SKETIEKYLMDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIID
RAVGAPIERPKSFSTEKYKELVKKIESKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRFRGRTIPELORELPKAEGSTEPLPEALFWLLLTGEIPTDAOVKALSADLAARSEIP
EHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSAILSTISKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQT
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomyceaceae; Saccharomyces.

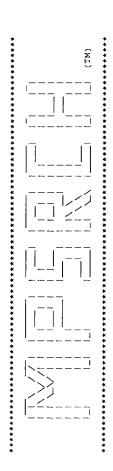
1 (bases 1 to 4391)
Aert,R., Verhasselt,P., Voet,M. and Volckaert,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-APR-1996) Data collected by MIPS on behalf of the European yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG, E-mail: Mewes@mips.embnet.org
1702 GGTGTGTTACCCCCAATTAATCATCGATAGGGCTGTTGGTGCTCCAATCGAAAGGCCCAAA 1760
                                                                                     1207 GGAATATGCTCACAGCTTATATGGGACCGAGCTCTTGGCTTGCCGCTAGAGAGGCCCAAA 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="anticodon gene: AGG; tRNA-Pro2 · common name" complement(3390. .3301) complement(3380. .38501) complement(3382. .3497)
                                                                                                                                                                            11-AUG-1997
                                                                                                                                                S.cerevisiae chromosome XIV reading frame ORF YNROOLC. 271616 Y13139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
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/gene="tP(AGG)NR - systematic name"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"SWISS-PROT:P00890"
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/note-"CEN element CDE III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CEN element CDE I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA96277.1"
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/db_xref="G1:1302469"
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complement(3503, .3873)
/note="solo-tau"
3983, .4056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SGD:L0000341"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="XIV"
                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae
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142. 110
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                                                                                                                                                                                                                                                                    Z71616.1 GI:1302468
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                                                                                                                                                                                                                                                                                                              baker's yeast.
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gene //gene="tN(GTT)NR - systematic name" //note="anticodon gene: GTT; tRNA-Asn - common name" //note="anticodon gene: GTT; tRNA-Asn - common name" //gene="tN(GTT)NR - systematic name" //gene="tN(
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S q Cp qq Cp g Sp qq Cp qq Cp q Cb qq  $^{\rm Cp}$ qq S, qq Сb qq S qq  $^{\circ}$ qq g g Cp

1205 AGACTCCTTGATACCCCAAACAAAAACCGTATAGTATCTTGCTTCTGTCAAACCATAGTGG 1146 1184 TGCAATAAAACACCGGAATGTGAATCAACATTTGGCCATGGGTTCTTAGTTTTACCATGC 1243 1664 TCCTTGTTTTCGTAGCCCAAAAGTTGGGCCAAATTTTTACCATAGTCAGCATTAGGATCG 1723 1904 GAAAATTGGGCCATTGGATGTAGATCTTTTGGGAGGCTATCTAAAAGTTGGATAACGTGC 1963 1964 TCTGGAATTTCTGATCTGGCAGCTAAATCAGCAGAAAGGGCTTTAACTTGAGCGTCAGTA 2023 TCTGGGAAATGTTTCAATGCGAATTCACGTTGAGCCGTATAACGAGGATCAGTTTTTCTC 1363 AAAACCGCATGGCCATAACCAGGAACAACTCTCCCTGCGTTCAAAGTATCCCACAAGTAC 1423 TITICAATIGITICITITGAATAGICACCITICACTICITCICICAATITAAATAGCCAT 1483 1484 TCTAAAACTTCTTGATTGGCACGACCATGTAATGGGCCAGCTAAACCATTCAAACCAGG 1543 GCCAAAGATAAGTATGGCGAAGATAAGGCAGAACCCACTAAATGTGTATGGGCAGAA 1603 ACGITACCACCITCAIGAICAGAAIGAAIAGITAAAIAIAGICICAITAAGTCAATAAAA 1663 1724 GTTGAAGTAATTTTACCATCCTTGAACACATTACGATAAATTTTGGAAGCAATAACAGGT 1783 1844 ACACCTIGAGCATATGCTTTGGCAAACTTAGACTTGGCTTTCTAAAGCAGTCACGGCAATA 1903 605 AGGGGTATTACTTGTCATTCTTATACATCCTCCGATAAACATAAGCTGCAACAACAGGA 546 965 AATACTCCTAGACCAAATCCAGGTACAACCTTGCCACTGTTTAGTGTCTTCCAAACATAA 906 905 TCTITCAACTGCTCTGTCGAGATGTTCTCTCCCACATTCATCAACAACTGATTTAATCCAC 846 725 ACATITICCACCTCATGATCACIGIGAATIGIGACATAAAGGCGCATCAGCTCAAGCATC 666 425 CAAAACTGAGTCATTGGATGAGCCGTAATAGGTAGAGCATCAATTGTTTTTGTACACATGG 366 1244 TIAGTIAAAACCCCTGGGGCAACTICATAAAIGGIGGAGACCAACTIAAAIAACTCGTAA 1085 TCTAATAGAATAGGAGGCACCACTTCATACAACTTTGACAACTTGAAAAATGGGTCA 845 AGCAGGACITCCIGGIIGGCIAAICCAIGGAGIGGCCCAGCCAAACCAITTAAIGCIGCI 545 ACTIGAGCAATCAAACTAAGGCAGTCCTCATAIGTIGGCTCCCAAAACTITGACTTATGG 485 ATCCCTTTCTCATATGCCTTCTGAAATTCGCTTCGAGTCTGTAAGGCCATAACACCAGTG 1364 1544 1604 1304 1424

Search completed: Sat Oct 23 18:29:06 1999 Job time: 2834 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit.

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MasPar time 351.57 Seconds 945.291 Million cell updates/sec n.a. - n.a. database search, using Smith-Waterman algorithm Sat Oct 23 19:14:04 1999; MPsrch\_nn Run on-

Tabular output not generated

Title:

>US-08-702-718-3 (1-1551) from US08702718.seq 1551 Description: Perfect Score: N.A. Sequence:

....AAAAAAAAAAAAAAAA 1551 1 TCCTCTAACCTTGACCTTCG...

TABLE default Gap 6 Scoring table:

271905 seqs, 107135622 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq35

Mean 9.510; Variance 7.769; scale 1.224 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

No. Score Match Length DB 1 1551 100.0 1551 16 2 764 42.8 1891 17 5 42.2 2.7 204 1 5 42.8 2.7 204 1 6 42.8 2.7 204 1 7 39 2.5 91 9				
0444 00444 000444444	Length DB	ID	Description	Pred. No.
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00000 7.7.0.00	1891 16		Potato citrate syntha	0.00e+00
4444 7.000	204 1		Base substituted E.co	3.09e-06
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,	91 9		Oligonucleotide probe	5.63e-05
,	91 9		Oligonucleotide probe	1.46e-04
	1077 46		Human tumour necrosis	2.46e-03

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Nucleotide sequence of Generic DNA sequence Generic DNA sequence Nucleotide sequence Nucleotide sequence Human G protein gamma Arabidopsis STZ polyphono sapiens CT44.2 Secreted protein BD38 Tomato hap80 cDNA seq Primer used in the la 3' nucleotide sequence Clone BV66.1 coding splasmid pMG3C9 used the Tat UBCE2A coding sequence encoding ins Human buiquitin conjustument buiquitin conjustument build motor neuron Human survival motor neuron Human survival motor neuron Human survival motor Survival motor neuron Human clongerase revellowtail tuna DNA ellowtail tuna DNA ellowtail tuna DNA ellowtail in DNA replica Generic DNA sequence Human famunodeficience Mammalian DNA replica Generic DNA sequence PNA)	e mouse beta-actin
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# ALIGNMENTS

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DNA encoding plant citrate synthase - used to regulate flower formation,
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Claim 6; Page 57-60; 87pp; English.

Claim 6; Page 57-60; 87pp; English.

To identify a cDNA from sugar beet which codes for citrate synthase, a class contained to the companient of the companient of the strength of the companient of solution to the companient of the clones was sequenced. The nt. sequence is given in T04200.
                                                                                                                                                               14.5EP-1995.
07.MAR-1995.
08-MAR-1994; DE-408629.
22-SEP-1994; DE-435366.
19-0CT-1994; DE-438821.
19-GRE ) HOECHST-SCHERING AGREVO GMBH.
La Cognata U, Landschutze V, Muller-rober B, Landschuetze V; Mueller-roeber B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 G;
                                          25-13N-1996 (first entry)
Sugar beet cirrate synthase CDNA.
Citrate synthase; flower formation; ss.
Beta vulgaris strain Zuchtlinie 58 0026
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 C;
                T04200 standard; cDNA to mRNA; 1551 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1551 BP;
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                                 T04200;
RESULT
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Similarity Sil: Consert Conser	imilarity Conser Conser Taacettga Taacetga Taace	Jas. Fred. NO. 4.008-00; Je 0; Mismatches 0; Indels 0; G. egttcagagttacaagaactgattcctgaacaacaggaacg:		aaagaatttggaagtttccagctgggaatatcaatgttgacatg 120 	aggaatgactggtttactttgggagacttccttactcgaccca 180 	tcaggggtttttctatacctgaatgccagaaacttttacccgct 240	agccattgcctgaaggtcttctttggcttctttaaccggaaag 300 	gtagatgctctatcagcagatttacgaaaacgtgcttctatc 360 	nacaattgatgctctacctattacggctcatccaatgactcag 420 	gocttacagactcgaagcgaattcagaaggcatatgagaaa 48) 	<pre>jtttgggagccaacatatgaggactgccttagtttgattgct 540                                     </pre>	gcttatgtttatcggaggatgtataagaatggacaagtaata 600 	octtgattatggtggaaatttcgcacacatgttgggatttgatagc 560 	jatgcgcctttatgtcacaattcacagtgatcatgagggtgga 720 	ctggccatttggtggtagtccactttcagatccttattgtca 780 	sgtttggctgggccactccatggattagccaaccaggaagtc 840 	ngttgttgatgaatgtggagagaacatctcgacagagcagttg 900 	gaagacactaaacagtggcaaggttgtacctggatttggtctagga 960 	Caagatacacatgccaaagagaatttgcgttgaagcacttg 10 	JUAAGATAUAUATGUUAAAGAATTTGUGTTGAAGUAUTTG 102
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DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting claim 7. Page 60-63; 87pp; English.

To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solamm tubersum citrate synthase cDNA (104199). One of the clones was sequenced. The nt. sequence is
ccaaagagtgtcactatggaatggcttgaaaagttttgtaaaagaagagcataacattga 1320
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Mueller-roeber B;
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Citrate synthase; flower formation; ss.
Nicotiana tabacum
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TO4201 standard; cDNA to mRNA; 1747 BP.
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19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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07-MAR-1995; E00859.
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                     1 TCCTCTAACCTTGACCTTCGTTCAGAGTTACAAGAACTGATTCCTGAACAACAGGAACGA 60
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P-PSDB; R86383.
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Citrate synthase: inhibitor; increased storage capacity: potato;
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19-CCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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T03410 standard; cDNA; 1891 BP.
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443 aaggtettetetggettettttaacaggaaaggtgecatcaaaagagcaagtgaatteaa 502
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DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting to improve storage of tubers, etc. and to reduce sprouting to improve storage of tubers, etc. and to reduce sprouting of an expensive spring in a cDNA from potato which codes for citrate synthase, a cDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos T04.02 and T04.03 which are complementary to the 5 or 3 or of or five coding region of A. thaliana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. The nt sequence is given in T04199. Sequence 1891 BP; 512 A; 370 C; 425 G; 584 T;
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                                                                                                              Potato citrate synthase cDNA.
Citrate synthase; flower formation; tuber storage;
Solanum tuberosum.
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09-MAR-1994; DE-408629.
22-28P-1994; DE-435366.
19-CCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
LT 4
104199 standard; cDNA to mRNA; 1891
104199;
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Best Local Similarity 78.5%;
Matches 997; Conservative
                                                                                      25-JAN-1996 (first entry)
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1043 tagaagaatgtgggggagaacatttccaaagagcagttgaaagactatgtttggaaacat 1102
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                                                                                                                                                                                                                                                                                                                                                                                          1163 gatatacatgccagagagttcgctatgaagcatttgcctgaagatccactgtttcaac 1222
                                                                                                                                                                                                                                                                                                                                                                                                                    983 GATACACATGCCAAAGAGAATTTGCGTTGAAGCACTTGCCTGATGACCCATTTTTTCAAT 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                              1223 tggtttcaaaaactctacgaagtttt-cctcctgttcttacagaacttggcaaagttaa-a 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1281 a-cettggccaaatgttgatgcccacagtggtgttgttgatgaactattatggtttaactg 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1340 aagcaagatattatacggtcctctttggcgtatcaagagctcttggcatttgctctcagc 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1163 AAGCAAGATACTATACGGTTTTGTTTGGGGTATCAAGGAGTCTTGGAATATGCTCACAGC 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    983 tagocogaaccacttcatggtttagccaatcaggaagttttgctatggataaaatctgttg 1042
                                                                           922
                                                                                                                                            923 acttggttgctagtgctttgtctgatccttacctctcctttgctgctgctttgaatggtt 982
                                                                                                                                                                                                863 ITGATGAATGTGGAGAGACATCTCGACAGAGCAGTTGAAAGATTATGTTTGGAAGACAC 922
                                                                                                                                                                                                                                                                                                                                                                 923 TAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAA 982
                         743 tttatcgcaggatgtacaagaatggtgacactatacctaaggatgaatccctggattatg 802
                                                  566 TTTATCGGAGGATGTATAAGAATGGACAAGTAATACCGCTGGATGACTCCCTTGATTATG 625
506 AGCCAACATATGAGGACTGCCTTAGTTTGATTGCTCAAGTTCCTGTTGTTGCAGCTTATG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggctctatgtaacaatacacagtgatcatgaaggtggtaatgtcagtgctcacaccaggtc
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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187..204
/*tag= b
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1987; US-034819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1460 ggcttgagaa 1469
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30-MAR-1988; 105163.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  778 TCATTTGCAGCAGCATTA-AATGGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lehtovaara P, Knowles J, Koivula A, Bamtord J, Kelnikaineu i, WPI: 88-27927740.
Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                           Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
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Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are mishncorporated by the transcriptase and the molecules are completed to forms that can be amplified and them expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                             transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.

See also P80575.
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08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 yvybbbvynvhnhnnenecebnnhvchnvhbnnhrnwayvrhdarrddvheeveh 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           837 AGTCCTGCTGTGGATTAAATCAGTTGTTGATGAATGTGGAGAACATCTCGACA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 Others;
                                                                                                         Disclosure; p; English.
Random point mutations were introduced into the alpha fragment of E.coll beta-galactosidase. The wild type sequence was obtained single stranded template and an oligonucleotide was hybridised it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen WPI; 88-279927/40.
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Pred. No. 3.09e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 C; 17 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/function=multiple cloning site
187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1; I
Pred. No. 3.09e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                   17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 occurred singularly in any given mutant.
See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
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N81164 standard; DNA; 204 BP
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10.1%;
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Best Local Similarity 12.2%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              204 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 A;
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30-MAR-1988; 105163
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
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Matches

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Indels

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Thuman tumour necrosis factor receptors 6-alpha and 6-beta - used in the diagnosis of immune system related disorder(s)

Disclosure; Fig 1: 91pp; English.

The diagnosis of immune system related disorder(s)

Disclosure; Fig 1: 91pp; English.

The invention also provides

The present sequence represents the human tumour necrosis factor

receptor-6 alpha (TNRP-6 alpha) cDNA. The invention also provides

for the TNRP-6 beta cDNA (V39086). TNRP-6 alpha and TNRP-6 beta are

members of the tumour necrosis factor receptor (TNRP) family. TNRRs

are expressed in endothelial cells, keratinocytes, normal prostate and

particularly of the immune system, substantially altered (whether increased or decreased) levels of TNRP-6 alpha and/or TNRP-6 beta gene expression can be detected, therefore the TNRP-6 alpha and TNRP-6 beta collypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNRP-6 alpha and TNRP-6 beta genes can also be detected. The TNRP collypeptides are claimed to be useful for identifying ligands which may be useful in the treatment of apoptosis related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour necrosis factor receptor-6 alpha cDNA.
Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1998 (first entry)
Nucleotide sequence of tumnour necrosis related receptor (TR4).
Human, tumnour necrosis related receptor; TR4; agonist; antagonist;
inhibition; chronic; acute; inflammation; arthritis; septicaemia;
autoimmune disease; transplant rejection; stroke; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial cells; keratinocytes; normal prostate; apoptosis; prostate tumour tissue; ss.
Homo sapiens.
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                                                                                                                                                                        268 CAGGCAATGGCTCTGCACCAGCACTTGCAGCGGGTAAAAGTTTCTGGC 221
                                                                                                         13 vhsyyvvhvvshhhsvhhvvhhvhvsvvvhhvvhvvhhvhyhvyvsv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 G;
       Pred. No. 1.46e-04;
43; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "INFR-6 alpha protein"
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111..1013
                                                                                                                                                                                                                                                                      T 9
V39085 standard; cDNA; 1077 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
Ebner R, Feng P, Gentz RL, Ni
WPI; 98-399142/34.
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Best Local Similarity 94.9%;
Matches 37; Conservative
Best Local Similarity 0.0%;
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1998 (first entry)
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13-JAN-1998; UO0153.
14-JAN-1997; US-0354
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0
                                                                  92 hhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnnc 151
                                                                                                                                 843 CAGGACTTCCTGGTTGGCTAATCCATGGAGTGGCCCAGCCAAACCATTTAATGCTGCTGCTGC 784
   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonuclectide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP: 5 A: 17 C: 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
   56; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 2.5%; Score 39; DB 9; Length 91; Best Local Similarity 0.0%; Pred. No. 5.63e-05; Matches 0; Conservative 41; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 CITITAACCGGAAAGGIICCIAGCAAAGAGCAAGIAGAIGCIC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 vhsyyvvhvvshhhsvhhvvhhvhvshvvhhvvhhvhyh 55
                                                                                                                                                                                                       152 ncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvch 190
                                                                                                                                                                                                                                                                      783 AAAIGACAAAIAAGGAICIGAA-AGIGGACIACCCACCA 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                             Q51746 standard; cDNA; 91 BP.
Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q51746 standard; cDNA; 91 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BECT ) BECTON DICKINSON CO. Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BECT ) BECTON DICKINSON CO.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%;
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EP-571911-A.
01-DEC-1993.
24-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 14; 23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-1992; US-889651.
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WPI; 93-378844/48.
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24-MAY-1993; 108325.
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   10;
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samples

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Gaps

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2; Indels

Query Match

samples

ID DAY COLOR COLOR

195 T;

US-08-702-718-3.rng

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identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; page 35, 255pp; English.

Old 68 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11/TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specific peptides generated by these generic sequences are shown in R6515-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions — a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or blologically active.They may further comprise a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                 and prevent e.g. inflammation, arthritis, septicaemia, autoimmune diseases, transplant rejection, infection, stroke, ischaemia, ARDS, restenosis, AIDS, bone disorders and cancer.

Claim 3: Fig 1: 21pp: English.

This is the nucleotide sequence of the human tumour necrosis related receptor (TR4), used in the method of the invention. The TR4 protein or its agonist can be used to treat a subject in need of enhanced TR4 polypeptide activity. The antagonist is used to inhibit TR4 polypeptide activity. The active agents can be used for the treatment and prevention of diseases such as chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases, transplant rejection, stroke, cancer, Alzheimer's disease.

Sequence 1164 BP: 206 A; 396 C; 355 G; 207 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                  New DNA encoding tumour necrosis related receptor - used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
//note= "this sequence represents 'Z'; Z can be a
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 2.3%; Score 35; DB 49; Length 1164;
Local Similarity 94.9%; Pred. No. 2.46e-03;
Nes 37; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1116 ataaagctttttcataaaaaaaaaaaaaaaaaaaaa 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1513 ATAAAAATTTTCATAAAAAAAAAAAAAAAAAAAAA 1551
                 /product= "human TR4"
                                                                                                                                      Emery J, Tan KB, Truneh A, Young PR; WPI; 98-508248/44.
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                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
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Q70468 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNC-) UNIV NORTH CAROLINA. Fowlkes DM, Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1995 (first entry)
                                            20-JAN-1998, 200382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1993; US-013416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1993; US-176500.
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                                                                                                                                                          WPI; 98-508248,
P-PSDB; W66102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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resols notifying proteins or peptide(s) which bind a ligand - by
recombinant vector library expressing fusion proteins
comprising a recombinant vector library expressing fusion proteins
comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.

70765 is a generic DNA sequence used to generate random TSAR (Totally
Synthetic Affinity Respents) peptides. This generic formula can also be
represented as follows: X(NNB)6 (TGC)(NNB)12 (NNB)14 (TGC)(NNB)3Y. X
and Y are flanking restriction sites (X is not the same as Y) that are
not specified further. Other generic sequences are shown in
R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
comprising at least two functional regions - a binding domain with
R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
comprising at least two functional regions - a binding domain with
chemically or biologically active. They may further comprise a linker
peptide between the 2 domains. The oligonuclectides are also designed so
that the expressed peptide contains. 2 or 4 cysteine residues positioned
in, or flanking, the unpredicted or variant residues. These residues
confer some degree of conformational rigidity to the peptides. The TSARs
correct comprising a TSAR binding domain can be used in vivo to
deliver a chemically or biologically active moiety, eg. metal ion,
radioisotope, peptide, toxin or enzyme, to the specific target or on the
                  that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                          0
peptide between the 2 domains. The oligonucleotides are also designed so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 IIGGAIGAGCCGTAAIAGGIAGAGCAICAAIIGIIIIGIACACAIGGICIGGGAIAGAAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 bnabanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 CACGITITCGIAAAICIGCIGAIAGAGCAICIACIIGCICITIGCIAGGAAC 301
                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 32; DB 12; Length 114,
larity 3.6%; Pred. No. 3.84e-02;
Conservative 32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 12
Q70465 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UXNO-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q70465;
05-APR-1995 (first entry)
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P-PSDB; R65150 and R65151.
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                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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This is the nucleotide sequence of the clone CH377], used in the method of the invention involving secreted proteins from human cells potentially useful as immuno-modulators, anti-tumour agents, itssue growth promoters, haemostatic and thrombolytic agents. It was isolated from an adult human testes cDNA library. They may be used to express the recombinant protein, as tissue/molecular weight markers, for chromosome identification, to identify possible genetic disorders and isolate new related DNA, as sources of primers for PCR, to generate anti-PDR anti-DNA antibodies, or in interaction trap assays to identify sequences that encode interacting proteins.

Sequence 525 BP; 211 A; 104 C; 79 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1469 TICACITGTAAATATATIGTAIGGTITCIIGAICAAAAAAIGAGAIAAAAGAGIITICAIA 1528
cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-007-1998 (first entry)
Nucleotide sequence of the CH377_1 clone.
Clone CH377_1; secreted protein; human cell; immuno-modulator; PCR;
anti-tumour agent; tissue growth promoter; haemostatic agent; primer;
thrombolytic agent; molecular weight marker; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 ttctcctagtcaatatctttagtgatyttytttaataaacatgraagcaaagraaaaaaa 480
                                                                                                                                                                                                                                                                      Score 33; DB 46; Length 525;
Pred. No. 1.55e-02;
4; Mismatches 25; Indels 0; Gaps
                                                                                                                                                                                                                                          3 banbanbanbanbanbtgcanbanbanbanbanbanbanbanbanbanbanbananana 62
                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding secreted protein from human cells potentially useful, e.g. as immuno-modulators, anti-tumour agents, promoters of tissue growth, haemostatic and thrombolytic agents claim 37; Page 77; 98pp; English.
                                                                                                                                                                                                                                                                                                                            88 ITCCAAATICTTTCTTTATCTTCAGTCGTTCCTGTTGTTCAGGAATCAG 37
                                                                                                                                                       Length 114;
                                                                                                                                                                         Pred. No. 3.84e-02;
32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; WPI; 98-297936/26.
                                                                                                                                                         DB 12;
                                                                                                                                                         Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1529 AAAAAAAAAAAAAAAAAA 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  V41453 standard; cDNA; 525 BP.
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13-NOV-1997; US-969515.
15-NOV-1996; US-749745.
02-UUN-1997; US-867678.
(GEMY) GENETICS INST INC.
                                                                                                                                                     2.1%;
Similarity 3.6%;
4; Conservative
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Best Local Similarity 65.1%;
Matches 54; Conservative
                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1998.
                                                                                                                                                         Query Match
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                                                                                                                                                                                                 Matches
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Screen for agonists and antagonists of G protein interaction claim 1: Page 29; 40pp English.

CDNA clones (14769-75) respectively code for human G protein submara.2, gamma-2, gamma-7, gamma-7, gamma-10 and gamma-11 subunits (W09412-18). Several human cDNA libraries were partially sequenced to identify expressed sequence tags (EST). By matching sequences of EST to genes of known structure, the 7 new subunit sequences of EST to genes of known structure, the 7 new subunit has been deposited as APCC 97139. The cDNA clone for gamma-11 has been deposited as APCC 97139. The isolated cDNA clones can be used to horduce recombinant gamma subunits in prokaryotic or eukaryotic host cells for use in the development of therapeutic and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding gamma subunits of human G protein - used to detect mutation(s) in, or altered levels of, the subunits and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agents. The nucleic acids can also be used to produce probes to detect mutations in human G protein subunit sequences and for chromosome identification.
19-WAY-1997 (first entry)
Human G protein gamma-11 subunit cDNA.
G protein; signal transduction; agonist; antagonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 2.1%; Score 32; DB 29; Length 654; Best Local Similarity 76.7%; Pred. No. 3.84e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 C;
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEECHAM CORP.
(WEIS-) WEIS CENT RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 A;
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                                                                                                                                                   /*tag= b
330..654
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607..612
/*tag= d
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108..329
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                                                                                               .107
                                                                                                                                                                                                                                                                                 WO-006406
                                                                                                                                                                                                                                                                 22-MAY-1995; U06406.
22-MAY-1995; WO-U064
                                                                                                                                                                                                                                                                                                                                               Kunsch CA, Robish
WPI, 97-021140/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       654 BP;
                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; W09418
                                                                  Homo sapiens.
                                                                                                                                                                                                  polya_signal
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                                                  therapy; ss.
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CC 2 cDNA clones (T58281 and T58282) respectively code for the STZ (W01604) and STO (W01605) polypeptides of Arabidopsis thaliana. CC They were isolated by using clones of an A. thaliana cDNA library CC to transform yeast strains that lacked active calcineurin CC salt than wild-type strains). Clones that complemented the salt CC stl than wild-type strains). Clones that complemented the salt corp have the ability to confer salt tolerance analysis. STZ and CC fungi and other organisms. Recombinant expression cassettes incorporating the STZ or STO sequence can be used to produce CC transgenic plants able to grow under saline conditions. Sequence 940 BP; 289 A; 235 C; 186 G; 230 T;
```

Ouery Match 2.1%; Score 32; DB 28; Length 940; Best Local Similarity 69.0%; Pred. No. 3.84e-02; Matches 58; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 911 aaaaaaaaaaaaaaaaaaa 934

Search completed: Sat Oct 23 19:20:04 1999 Job time: 360 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch\_nn

MasPar time 112.95 Seconds 1187.596 Million cell updates/sec Sat Oct 23 19:20:21 1999; Tabular output not generated. Run on:

>US-08-702-718-3 (1-1551) from US08702718.seq 1551 Title:

Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

165359 seqs, 43243793 bases x 2 Searched:

Dbase 0; Query 0

..

STD

Nmatch

Post-processing: Minimum Match 0% Listing first 45 summaries

n-issued
1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 8.940; Variance 5.499; scale 1.626

Statistics:

# SUMMARIES

Q	Score	Match	Length	DB	ID	Description	Pred. No.
c 1	84	3.1	7218	~	US-08-232-	Sequence 14, Applicati	8.27e-14
C 3	35	e. 5	215	٦	US-08-238-	Sequence 5, Applicatio	1.88e-05
3	32	2.1	654	4	PCT-US95-0	11,	7.54e-05
7	32	2.1	940	m	US-08-471-	1, A	7.54e-05
Ŋ	32	2.1	965	٣	US-08-388-	Çį	7.54e-05
9	31	2.0	208	7	US-08-686-	Sequence 37, Applicati	2.52e-04
7	31	2.0	1046	Н	US-08-361-	Sequence 4, Applicatio	2.52e-04
80	31	2.0	1046	m	US-08-484-	Sequence 4, Applicatio	2.52e-04
6	31	0.2	1137	٣	-904-80-sn	ci	2.52e-04
10	31	0.3	1856	m	-904-80-SD	εł	2.52e-04
11	31	0.	2589	4	PCT-US96-1	Sequence 1, Applicatio	2.52e-04
15	31	0.7	5173	7	US-08-242-	ı,	2.52e-04
13	30	1.9	41	Н	US-08-113-	39,	8.31e-04
14		1.9	44	~	US-08-113-	40,	8.31e-04
15	e	1.9	55	-	US-08-113-	41,	8.31e-04
16	2	1.9	92	-	US-08-120-	94,	2.70e-03
17	29	1.9	92	m	US-08-478-	94	2.70e-03
18	29	1.9	97	m	US-08-478-	Sequence 87, Applicati	2.70e-03
19	29	1.9	97	r-4	US-08-120-	Sequence 87, Applicati	2.70e-03
02	53	1.9	140	-	ns-08-628-	Sequence 5, Applicatio	2.70e-03

2.70e-0.3 2.70e-0.3 2.70e-0.3 3.11e-0.4 3.11e-0.4 2.70e-0.3 3.11e-0.4 2.70e-0.3 3.66e-0.3 8.66e-0.3 8.66e-0.3 8.66e-0.3 8.66e-0.3 8.66e-0.3 8.66e-0.3 8.66e-0.3 8.66e-0.3 8.66e-0.3
Sequence 6, Application Sequence 19, Application Sequence 17, Application Sequence 27, Application Sequence 27, Application Sequence 22, Application Sequence 6, Application Sequence 1, Application Patent No. 5378464.  Sequence 1, Application Sequence 21, Application Sequence 1, Application Sequence 21, Application Sequence 13, Application Sequence 14, Application Sequence 15, Application Sequence 16, Application Sequence 17, Application Sequence 18, Application Sequence 19, Application Sequence 3, Application Sequence 3, Application Sequence 19, Application Sequence 21, Application Sequence 3, Application Sequence 21, Application Sequence
US-08-628- US-08-686- US-08-554- US-08-226- US-08-238- US-08-29- US-08-29- US-08-29- US-08-29- US-08-29- US-08-29- US-08-138- US-08-138- US-08-138- US-08-178-
1244883388483442348441444444444444444444
240 358 5731 684 684 687 687 688 687 688 687 688 687 688 687 688 688
88888888888888888888888888888888888888
0 0 0 10 10 10 10 10 10 10 10 10 10 10 1

## ALIGNMENTS

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                           Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30472/114 IMMU
CLEAR STETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY, PAGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                               AUDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                          XXXXXX
 RESULT
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Gaps

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| 507 GCCAACATATGAGGACTGCCTTAGTTTGATTGCTCCAAGTTCCTGTTGTTGCAGCTTA-TG 565
                                                                                                                                                                                                                                                                                                                                              68 YGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAM 127
                                                                                                                                                                                                                                                                                                                                                                        566 ITTATCGGAGGATGTATAAGAATGGACAAGTAATACCGCTGGATG-ACTCCCTTGATTAT 624
                                                                                                                                                                                                                                                                                      8 SSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application PC/TUS9506406A
Sequence 11, Application PC/TUS9506406A
GENERAL INFORMATION:
APPLICANT: Janet D. Robishaw, Charles Kunsch
TITLE OF INVENTION: CDNA Clones Encoding Human G Protein
TITLE OF INVENTION: Subunits
NUMBER OF SEQUENCES: 23
                                                                                                                                                          LOCATION: 1..215
OTHER INFORMATION: /Standard_name- "Deduced amino acid OTHER INFORMATION: Sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                             Match 2.3%; Score 35; DB 1; Length 215; Local Similarity 15.9%; Pred. No 1.88e-06; es 25; Conservative 67; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   128 TSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNS 164
                                                                                                                                                                                                                                                                                                                                                                                                                              625 GGTGGAAAİTTCGCACACATGTTGGGATTTGATAGCC 661
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PCT-US95-06406A-11 STANDARD; DNA; UNC; 654 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                           SEQUENCE CHARACTERISTICS:
                                                        215 base pairs
                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herewith
                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM 486
                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                    TOPOLOGY:
                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       1368 CTATATTATTGTAGATTCGACAAGAACAGTGAGTTGATGATATGTCATCAATGTTATGC 1309
                                                                                                                                                                                                                                                                                      1308 TCTTCTTTTACAAAACTTTTCAAGCCATTCCATAGTGACACTCTTTGGCCTCTCTAGGGGG 1249
                                                                                                                                                                                                                                                                                                                                              1248 CAAGCCAAGACTCGGTCCCATATAAGCTGTGAGCATATTCCAAGACTCCTTGATACCCC 118º
                                                                                                                                                                                                                                                                                                                                                                                                     1188 AAACAAAACCGTATAGTATCTTGCTTCTGTCAAACCATAGTGGTTCAGCAAAACTCCACT 1129
                                                                                                                                              Gaps
                                                                    CLONE: PIZ9PL-FIS
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                              DB 2; Length 7218;
8.27e-14;
                                                                                                                3.1%; Score 48; DB 2; Length 7218
Similarity 0.6%; Pred. No. 8.27e-14;
2; Conservative 195; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1128 ATGAGCATCAACATTAGGCCATGGATTCTTTACCTTTCCAAGGTCT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .T. 2
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LABAVITCH, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                        IMMEDIATE SOURCE:
                                                                                                                 Query Match
Best Local Similarity
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                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                                                                                                                                              Matches
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Query Match 2.1%; Score 32; DB 4; Length 654;
Best Local Similarity 76.7%; Pred. No. 7.54e-05;
Matches 46; Conservative 0; Mismatches 14; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                  APPLICANT: Gasser, Charles S.
APPLICANT: Lippuner, Veronica
TITLE OF INVENTION: GENES CONFERRING SALT TOLERANCE AND
TITLE OF INVENTION: THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 3; Length 940;
Pred. No. 7.54e-05;
0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 55..738
SEQUENCE 940 BP; 289 A; 235 C; 186 G; 230 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,717 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 ATTONBEY/AGBYI INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                  SEQUENCE 654 BP; 231 A; 116 C; 142 G; 165 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                JT 4
US-08-471-717-1 STANDARD; DNA; UNC; 940 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2307E-606
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              Sequence 1, Application US/08471717
Sequence 1, Application US/08471717
Patent No. 5859337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911 AAAAAAAAAAAAAAAAAAAA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 940 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 2.1%;
Best Local Similarity 69.0%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
NTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             STREET: One Market P
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    X: USA
94105-1492
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linea
MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                           XXXXXX
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1153 GGTTTGACAGAAGCAAGATACTATACGGTTTTGTTTGGGGGTATCAAGGAGTCTTGGAATA 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                      Sequence 22, Application US/08388672A
Sequence 22, Application US/08388672A
Patent No. 5795961
GENERAL INFORMATION:
APPLICANT: Wallace, T. Paul
APPLICANT: Carr, Frank J.
APPLICANT: Old, Lloyd J.
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 3; Length 965;
Pred. No. 7.54e-05;
44; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          836 ADTSSNSRSSVTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVS 878
.r 5
US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP.
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,672A
FILLING DATE: 14-FEB-1995
CLASSIFFCATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, No. 5795961man D.
REGISTRATION NUMBER: 30,946
REPRENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-888-9200
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  Felfe and Lynch
                                                                                                                                                                                                                            805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 965 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 21.4%;
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                        STREET: BULLITY: New York
                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                   ADDRESSEE:
                          XXXXXX
В
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.T 6 US-08-686-878A-37 STANDARD; DNA; UNC; 208 BP.

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CCEPACO

Sequence 37, Application US/08686878A Sequence 37, Application US/08686878A Patent No. 5708157

US-08-702-718-3.rni

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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET P O BOX 1404 CITY: Alexandria
                                                                                                                                        MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     992 AAAAAAAAAAAAAAAAA 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
IMMEDIATE SOURCE:
                                                            Virginia
: United States
                                                                                                                     COMPUTER READABLE FORM:
                                                                             COUNTRY: United ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE
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    1476 GTAAATATATTGTATGGTTTCTTGATCAAAACATGAGATAAAGAGTTTTCATAAAAAAA 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 GTAANTTTGTCNGNNGATAAATTGAANATAACNGNGATTAANGNNTNATGNTAAAAAAAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: De Greef, Willy
APPLICANT: De Greef, Willy
APPLICANT: Van Enmelo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria Helena
APPLICANT: De Souza, Maria Helena
APPLICANT: Van Montagu, Maria Helena
TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
TITLE OF SEQUENCES: 13
CORPESPONDENCE: ADDRESS:
                                                                                      APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Chery a
APPLICANT: Evans, Chery
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: TO SECRETE AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: TO SECRETE AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: TO SECRETE AND SECRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patenth Pelease #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/686,878A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
SEQUENCE 208 BP; 109 A; 12 C; 23 G; 43 T; 21 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 2; L
Pred. No. 2.52e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .T 7
US-08-361-467B-4 STANDARD; DNA; UNC; 1046 BP.
                                                                                                                                                                                                                                                       ADDRESSEE Genetics Institute, Inc
STREET: 87 CambridgePark Drive
CIIY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08361467B Sequence 4, Application US/08361467B Patent No. 5633441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BROWN. SCOLE A:
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 496-8824
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 37.
SEQUENCE CHARACTERISTICS:
                                   McCoy, John
LaVallie, Edward
Racie, Lisa
                    Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 208 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%;
Local Similarity 61.8%;
les 47; Conservative
                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
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02140
                    Jacobs.
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    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                           APPLICANT:
APPLICANT:
                  APPLICANT :
APPLICANT :
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                            APPLICANT:
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1469 TTCACTTGTAAATATATTGTATGGTTTCTTGATCAAAACATGAGATAAAGAGTTTTCATA 1528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/0848433C
Sequence 4, Application US/0848433C
Patent No. 5767374
GENERAL INFORMATION:
APPLICANT: De Greef, Willy
APPLICANT: Van Emmelo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria-Helena
APPLICANT: Van Montagu, Marc
APPLICANT: Van Montagu, Marc
TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

2.0%; Score 31; DB 1; Length 1046;
Best Local Similarity 60.8%; Pred. No. 2.52e-04;
Matches 87; Conservative 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER
SOFTWARE: Patentin Release #1.0, Version #1.30 CUPPENT APPLICATION DATA.
APPLICATION NUMBER: US/08/361,467B FILING DATE: 22-DEC-1994 CLASSIFICATION: 800
                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 8
US-08-484-332C-4 STANDARD; DNA; UNC; 1046 BP.
                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31.196
REFERENCE/COCKET NUMBER: 010830-027
TELECOMUNICATION INFORMATION:
TELECHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 89 402 224.3 FILING DATE: 04-A0(1-1989 ATTORNEY/AGENT INFORMATION: NAME: Schulman, Robert M
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Gaps

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ANTI-SENSE: NO FEATURE:
                                                                                                          63102
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                 COUNTRY:
                                                                                 CITY: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         872 AAGCAAAGAGAAAGAACGTAGTTTTCTTGTTTTCCTATTTTGTTTTCTCTCTATCAAAC 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.0%; Score 31; DB 3; Length 1045; 50.8%; Pred. No. 2.52e-04; atlive 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER.
                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,332C
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/361,467
FILING DATE: 22-DEC:1994
PRIOR APPLICATION DATA:
                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STRETT: P.O. Box 1404
CITK: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-706-214-2 STANDARD; DNA; UNC; 1137 BP.
                                                                                                                                                                                                                                                                                      NAME: Schulman, Robert M.
REGISTRATION NUMBER: 31,196
REFERENCE/DOCKET NUMBER: 010830-093
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISCIS:
LENGTH: 1046 base pairs
                                                                                                                                                                                                    APPLICATION NUMBER: US 07/681,492
FILING DAME: 04.APR.1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01.AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08706214 Sequence 2, Application US/08706214 Patent No. 5770720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              992 AAAAAAAAAAAAAAAAA 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1529 AAAAAAAAAAAAAAAAAAAAAA 1551
                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: 3C9
TITLE OF INVENTION: EMBRYOS NUMBER OF SEQUENCES: 13 CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                     STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.8%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXX
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Gaps
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Sequence 1, Application US/08706214
Patent No. 5770720
GENERAL INFORMATION:
APPLICANT: Deaul, Thomas F.
APPLICANT: Mang, Zhoa-Yi
APPLICANT: Shenk, Thomas E.
TITLE OF INVENTION: UBLQUITIN CONJUCATING ENZYMES HAVING
TITLE OF INVENTION: TRANSCRIPTIONAL REPRESSOR ACTIVITY
NUMBER OF SEQUENCES: 4
APPLICANT: Deul, Thomas F.

APPLICANT: Wang, Zhoa-Yi
APPLICANT: Shenk, Thomas E.

IIILE OF INVENTION: UBIGUITIN CONJUCATING ENZYMES HAVING
TITLE OF INVENTION: TRANSCRIPTIONAL REPRESSOR ACTIVITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul A. Stone, Esq.
STREET: One Metropolitan Square, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
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LOCATION: 88..564
SEQUENCE 1137 BP; 294 A; 285 C; 275 G; 283 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                  SCFUWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,214
FILING DATE: 30-40G-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 3; Le
Pred. No. 2.52e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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US-08-706-214-1 STANDARD; DNA; UNC; 1856 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,040
FILING DATE: 21-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,995
FILING DATE: 30-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JWH 10033
                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNATION NUMBER: 38,628
REGISTRATION NUMBER: 38,628
REFERDOMUNICATION INFORMATION:
TELEPOOMUNICATION INFORMATION:
TELEPOOMUNICATION 1314,231-5400
TELERX: (314) 231-5400
TELERX: (502697583 MCI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.0%;
Best Local Similarity 89.7%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                     STREET: One Meta
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SEQUENCE CHARACTERISTICS:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco CITY: San Francisco CITY: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                              Length 1856;
                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 807..1283
SEQUENCE 1856 BP: 401 A; 499 C; 518 G; 438 T; 0 OTHER.
                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,214
FILING DATE: 30 AUG-1996
       E: Paul A. Stone, Esq.
One Metropolitan Square, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                 1809 ATAAACTGTTTATAAAAAAAAAAAAAAAAAAAAAAAA 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9612860
Sequence 1, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INFORTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 2.0%; Score 31; DB 3; Lv Best Local Similarity 89.7%; Pred. No. 2.52e-04; Matches 35; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .T 11
PCT-US96-12860-1 STANDARD; DNA; UNC; 2589 BP
                                                                                                                                                                                                       NAME: Stone, Paul A.
REGISTRATION NUMBER: 38,628
REFRENCE/DOCKET NUMBER: JWH 10033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 231-5400
TELEFAX: (314) 231-4342
TELEX: 6502697583 MCI
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                      FILING DATE: 30-NG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,040
FILING DATE: 21-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,995
FILING DATE: 30-AUG-1995
ATTORNEY AGENT INFORMATION:
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                      LENGIH: 1856 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
COPRESPONDENCE ADDRESS:
                        St. Louis
Missouri
                                                                                                                                                                                                                                                                                                                                                                   807.
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                                          USA
                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                  63102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111
        ADDRESSEE:
                                          COUNTRY:
                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
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Sequence 1, Application US/08242677
GENERAL INFORMATION:
APPLICANT: Wu, Foon W.
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: Treatment of AIDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: ALROIG, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.0%; Score 31; DB 4; Length 2589 Best Local Similarity 89.7%; Pred. No. 2.52e-04; Matches 35; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
SEQUENCE 2589 BP; 844 A; 436 C; 522 G; 787 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/242,677
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BEEZDEF, David J.

REGISTRATION NUMBER: 24,774

REGISTRATION NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:
TELEFAN: (415)781-1989

TELEFAN: (415)389-3249

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 12
US-08-242-677-1 STANDARD; DNA; UNC; 5173 BP.
                                                      UMBER: PCT/US96/12860
06 AUG 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-78-1400
TELEFARENCE: 713-780-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 713-70;
TELEPHONE: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                          APPLICATION NUMBER:
                                                                                              FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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5047 CACTITITIGITAAATIGIATICITICCTITAATAAAATAITITAAGCAATIGICCAATAAA 5105
                                                                                                                                                                                                                      1471 CACTTGTAAATATATTGTATGGTTTCTTGATCAAAACATGAGATAAAGAGTTTTCATAAA 1530
                                                                                                                                                                  0; Gaps
                                                                                                                                       Length 5173;
                                                                                 NAME/KEY: CDS
LOCATION: 1..4863
SEQUENCE 5173 BP; 1348 A; 1116 C; 1309 G; 1400 T; 0 OTHER.
                                                                                                                                       Score 31; DB 2; Length 5173;
Pred. No. 2,52e-04;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/08113646A
Sequence 39, Application US/08113646A
Patent No. 5578468
GENERAL INFORMATION:
APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
APPLICANT: PATEL, Dhavalkumar
APPLICANT: ANTCZAK, James B
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
RICHARD APPLICATION DATA:
APPLICATION NUMBER: US/07/084,406
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: RNA (genomic)
SEQUENCE 41 BP; 33 A; 2 C; 1 G; 0 T; 5 OTHER.
                                                                                                                                                                                                                                                                                                                     T 13
US-08-113-646A-39 STANDARD; DNA; UNC; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VIRGINIA
COUNTRY: U.S.A.
21P. 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOAPPY disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOKNEL/COLUMN
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE DOCKET NUMBER: 1579
TELECOMUNICATION INCRMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: 200797 NIXM UR
INFORMATION FOR SEC ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 5107 AAAAAAAAAAAAAAAA 5127
                                                                                                                                                                                                                                                                            1531 AAAAAAAAAAAAAAAAAAA 1551
LENGTH: 5173 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                       Match 2.0%;
Local Similarity 69.1%;
Les 56; Conservative
                                                    MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                           linear
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                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                  Matches
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Length 41;

DB 1;

1.9%; Score 30;

Query Match

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                            Gaps
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                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 1; Length 44; Pred. No. 8.31e-04;
                                                                                                                                                                                                                                                                                                             Sequence 40, Application US/08113646A
Sequence 40, Application US/08113646A
Patent No. 5578468
GENERAL INFORMATION:
APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
APPLICANT: ANTCZAK, James B.
TILLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
Best Local Similarity 80.6%; Pred. No. 8.31e-04;
Matches 29; Conservative 4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1516 AAGAGTTTTCATAAAAAAAAAAAAAAAAAAAAAAA 1551
                                                                                                              1516 AAGAGTTTTCATAAAAAAAAAAAAAAAAAAAAAAA 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) SEQUENCE 44 BP; 36 A; 2 C; 1 G; 0 T; 5 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AAAAGAUUUUAUAAAAAAAAAAAAAAAAAAAAAAAA 39
                                                                               4 AAAAGAUUUUAUAAAAAAAAAAAAAAAAAAAAA 39
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US-08-113-646A-41 STANDARD; DNA; UNC; 55 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                  J. 14
US-08-113-646A-40 STANDARD; DNA; UNC; 44 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/113,646A FILING DATE: 31-AUG-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/084,406 FILING DATE: 10-AUG-1987 ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLIL.
STATE: VIKGING.
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
-NUTTER: IBM PC COMPATIble
-NUTTER: IBM PC COMPATIble
-NUTTER: IBM PC COMPATIBLE
-NUTTER: IBM PC COMPATIBLE
-NUTTER: NUTTER: NUTTER: NUTTER: NUTTER: NUTTER: NUTTER: NUTTER: NUTTER: NUTER: NUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1579-20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/08113646A Sequence 41, Application US/08113646A Patent No. 5578468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELES: 200797 NIXN UR
INFORMATION FOR SED ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 1.9%;
Best Local Similarity 80.6%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXXX
                                                                                                                                                                                                                  RESULT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 1.9%; Score 30; DB 1; Length 55; Best Local Similarity 80.6%; Pred. No. 8.31e-04; Matches 29; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                       SOFTMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 13-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/084,406
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
GENERAL INFORMATION:
APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
APPLICANT: ANTCZAK, James B.
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES:
COPPESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
SEQUENCE 55 BP; 47 A; 2 C; 1 G; 0 T; 5 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AAAAGAUUUUAUAAAAAAAAAAAAAAAAAAAAAA 39
                                                                                                                                                                                                                                                                                                                                            FILLNO ATTORNEY AGENT INFORMATOL.

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

RECERENCE/FOCKET WINNER. 1579-20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELERAX: (703) 816-4100

TELERAX: (703) 816-4100

TELERAX: 200797 NIXN UP

INFORMATION FOR SEO ID NO: 41:

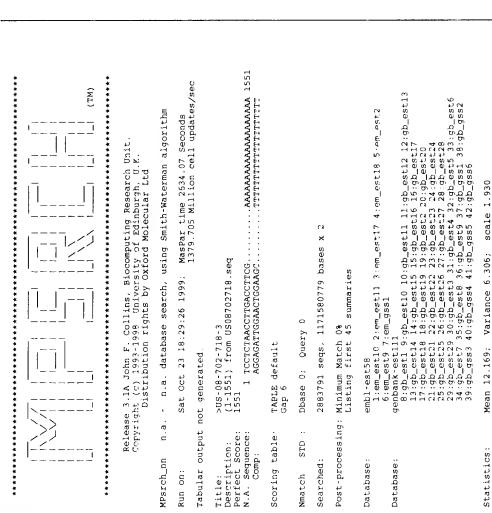
SEQUENCE CHARACTERISTICS:

LENGTH: 55 base pairs

TYPE: NUCleic acid

TYPE: Nucleic acid
                                                                                               ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC COMPATALIA
COMPUTER: IBM PC COMPATALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

Search completed: Sat Oct 23 19:22:19 1999 Job time : 118 secs.



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NO.	-189	-143	2-142	-126	-118	1.16e-115	-112	3.20e-108	26-6	06-á
Pred. No.	1.08€	2 470-143	9.57e-142	6.50e	5.06e-118	1.16€	9.836	8.20e	7.09e-97	1.17e-30
Description	L30-386T3 Ice plant La 1.08e-189	7448 Lambda-PFL2 Arabi	16899 Lambda-PRL2 Arab	EST220465 Normalized r	vm94h09.rl Knowles Sol	C96653 Rice callus Ory	16916 Lambda-FRL2 Arab	AU002699 Bombyx mori p	EST185581 Colon carcin	mx11d01.rl Soares mous
ID	AA896953	T44185	R90544	A1176862	AA606966	C96653	R90561	AU002699	AA313713	AA237580
DB	20	11	31	23	15	24	31	56	11	10
% Query Match Length DB	471	205	478	929	657	417	527	620	501	522
% Ouery Match	18.1	14.4	14.2	13.0	12.3	12.1	11.8	11.5	10.6	10.1
Score	281	223	C1	201	191	188	183	178	164	156
Result No.	Н	C1	m	4	S	9	7	œ	σ	10
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9.7 307 10 AA23170 466 36 AA11294 5 8.7 213 8 217455 8.7 252 17 AA73746 5 8.1 338 11 AA33746 1 7.8 489 23 A116870 7 7 418 34 W001297 7 7 444 10 AA24510 7 7 444 10 AA24510 7 7 7 444 10 AA24510 7 7 7 5 9 9 AA17472 8 7 7 5 343 21 AA9254 7 7 5 343 21 AA93254 7 7 5 452 9 AA19693 7 7 7 5 11 1 AA33501 7 7 7 8 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	7.4 506 26 AA901227 UI-R-AI dp-q-06-0-UI.S 1.66e-5 4 7.4 552 28 AI3238915 GH15054.5prime GH bross 1.66e-5 2 7.2 19134 W49861 ZEST00324 Maize Leaf, 5.31e-5 9 7.0 455 13 AA427173 ve83coll.rl Scares mous 9.46e-5 7 6.9 425 33 W14146 MD19e03.rl Scares mous 9.46e-5 5 6.8 302 12 AA356125 EST76627 Jurkat T-cell 9.23e-5 6 6 8 358 32 AA205271 ZQ71212.rl Stratagene 5.13e-5 6 6 5 8 555 22 AI05488 coau0002634 Cotton Bol 1.66e-5 6 6 5 8 56 15 AA568288 mull 166e-5 1 6.5 566 15 AA568281 mull 160e-3 1 6.5 566 15 AA568724 mull 160e-3 1 7.6 7.6 7.6 7.6 7.6 7.6 7.6 7.6 7.6 7.6	18953 19853 11ar 11ar 11ar 11ar 11ar 11ar 11ar 11a	Contact: Cushman JC Department of Biochemistry and Molecular Biology Oklahoma State University 350 Noble Pescarch Center, Stillwater, OK 74078-3035, USA Tel: 405-744-5207 Fax: 405-744-7799 Email: jcushman@biochem.okstate.edu PCR PRimers FORWARD: T7 PACKWARD: T3 Plate: L30-4 row: H column: 6 Seq primer. T3
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0.0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT LOCTS DEFINITIO NACCESSION NID VERYWORDS SOURCE ORGANIS AUTHORS ITILE JOURNAL	

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On Jan 7, 1998 this sequence version replaced gi:948518
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                                                                                 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
BCoRI, Site_2: XhoI"
/db_xref="taon:3544"
/clone="L30-386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          980 CAAGATACACATGCCAAAGAAAATTTGCGTTGAAGCACTTGCCTGATGACCATTTTTTC 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TIGIGGATGAATGIGGAGAAAACAICAGCAGGAGCAGGAGCIAAAAGAITAIGICIGGAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CATTAAAAAGTGGCAAGGTTGTACCTGGATATGGCCATGGAGTTCTGCGCAAGACGGATC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 AGAA-CCATGGCCGAATGTTGATGCCCACAGTGGGTGTATTGCTGAACTACTATGGTTTG 418
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7448 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123C9T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGTTGGCTGGCCCACTTCATGGATTAGCCAATCAGGAAGTGTTGCTGTGGATCAAGTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800 GTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTGTGGATTAAATCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860 TIGITGATGAATGTGGAGAACATCTCGACAGAGCAGTTGAAAGATTATGTTTGGAAGA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 GCCATTTGGTGGGTAGTCCACTTTCAGATCCTTATTTGTCATTTGCAGCAGCAGTAAATG 799
                                                                                                                                                                                                                                                                                                                                                                                                              1 GCCATTIGGIGGGIAGCGCACTTICAGAICCTTACCTTICATTIGCAGCTGCACTGAATG 60
                                                                                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                                                                                      /clone_lib="loe plant Lambda Uni-Zap XR expression
library, 30 hours NaCl treatment"
/tissue_type="Leaf, 30 h 0.4M NaCl"
                                                                                                                                                                                                                                                                                                                          Score 281; DB 20; Length 471; Pred. No. 1.08e-189;
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 65; Indels
                                                               /organism-"Mesembryanthemum crystallinum"
                                                                                                                                                                                                                                   /dev_stage="Six week old"
95 c 122 g 127
    High quality sequence stop: 320.
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                    Location/Qualifiers
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Arabidopsis thaliana
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Best Local Similarity 84.3%;
Matches 376; Conservative
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/note="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots: 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial issue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA clasers derived condity of primed cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   859 CTTGTTGATGAATGTGGAGAAGATCTCGACAGAGCAGTTGAAAGATTATGTTTGGAAG 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               799 GGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTGTGGATTAAATCA 858
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                                                                                          MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
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                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/strain="var columbia"
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90 c 118 g 149
                             MSU-DOE Plant Research Laboratory Michigan State University
                                                                                                                                                        Tel: 517-355-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7.
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                                                                                                                                                                                                                                                                                Location/Qualifiers
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Contact: Thomas Newman
                                                                                                                                                     17-353-0854
                                                                                                                           Lansing, Mi
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AI176862 676 bp mRNA EST 20-JAN-1999
EST220465 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 676)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
1060 GAAGIGGIGCCICC-TATICIATIAGAGCTI-GGAAA-GGIAAAGAAICCAIGGCCTAAI 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1266 CITIGGCCTCTCTAGCGGCAAGCCAAGAGCTCGGTCCCATATAAGCTGTGAGCATATTCC 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1206 AAGACTCCTTGATACCCCAAACAAAACCGTATAGTATCTTGCTTCTGTCAAACCATAGTG 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 CAGIGCCCTCGACACTCCGAACAGACTGTGTAGTAATTCATCTCCGTCATGCCATAGTA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 CTGGAGCAGCCCCACTGTGAGCATCTACGTTGGGCCAGGGGTTCTTAGCCTTTCCTTG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 CTTGGGCCTTTCTAGAGGGAAGCCTAGGGCTCTGCTCCAGATAAGCTGGGCCAACACACC 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jan 19, 1998 this sequence version replaced gi:2152042.
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188 c 150 g 181 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 201; DB 23; Length 676; Pred. No. 6.60e-126;
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/db_xref"*ATCC (inhost):2031570*
/db_xref"*taxon:10118"
/clone="ROVBX80"
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A1176862.1 GI:3727500
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Best Local Similarity 68.1%;
Matches 377; Conservative
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Unpublished (1998)
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                                                                                                                                                                                                                                                                             Retzel.E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant physiol. 106, 1241-1255 (1994) 95148729 On Apr 14, 1993 this sequence version replaced gi:693655.
                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes: Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 478)
                                                                                                                                                                                                                              Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
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Email: 22313tcn@ibm.cl.msu.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger
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/note="Organ: embryo: Vector: pSPORT: Site_1: Not1:
Site_2: Sall: Cloned undirectionally from mRNA prepared
from 800 blastocysts. Primer: Sall(dT):
5'-CGGTCGACCGTCGACCGTTTTTTTTTTTT-3'. CDNAS were
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AA606966
657 bp mRNA

EST
30-SEP-1997

DEFINITION vm94/b09.rl Knowles Solter mouse blastocyst Bl Mus musculus cDNA
clone IMAGE:1005953 5' similar to SW:CISY_PIG P00889 CITRATE
SYNTHASE, MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                        846 CAGCAGGACTTCCTGGTTGGCTAATCCATGGAGTGGCCCAGCCAAACCATTAATGCTGC 787
                                                                                                                                                                                                     906 AICTITCAACTGCTCTGTCGAGATGTTCTCTCCACATTCATCAACAACTGATTTAATCCA 847
966 CAATACTCCTAGACCAAATCCAGGTACAACCTTGCCACTGTTTAGTGTCTTCCAAACATA 907
                                                                                                                                                                                                                                           786 TGCAAATGACAAATAAGGATCTGAAAGTGGACTACCCACCAAATGGCCAGTGTGTGCACT 727
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                        On Sep 12, 1996 this sequence version replaced gi:1328460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="mouse blast./der_type="mouse blast./der_type="mbryo" (pre-implantation)" /lab_host="DHIOB" 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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/db_xref="taxon:10090"
/clone="IMAGE:1005953"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Poales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 CICITAGAGCAAGGGAAGGCIAAGAACCCIIGGCCCAACGIAGACGCICACAGIGGGGIG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 CGGGCACTGGGTGTGCTAGCCCAGCTCATCTGGAGCAGAGCCCTAGGCTTCCCCCTGGAA 603
                                                                                                                                                                                                                  660 cccrcagargcrrgagcrgargcccrrrargrcacarrcacagrgarcargagggrg 719
                                                                                                                                                                                                                                                                                          66 TAATGTAAGTGCCCACACAAGCCATTTGGTGGGGCAGCGCA-TTTCAGACCCTTACCTGTC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                     125 CTTTGCAGCAGCCATGAATGGGCTGGCGGGCT-CTACATGGACTAGCAAATCAGGAGGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 ATTIGCAGCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGT 839
                                                                                                                                              6 CCCTCAGIICACCGAGCICAIGCGIIIGIACCICACCAICCAIAGIGACCAIGAGGGIGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-0CT-1998
                                                                           Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS C96653 417 bp mRNA EST 19-UCT-19
DEFINITION C96653 Rice callus Oryza sativa cDNA clone C10531_5A, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            840 ccrccrcrcrcrcrarranarcactrcrrcarcangracacacacacacacacacacr
       Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Aug 21, 1998 this sequence version replaced
Score 191; DB 15; L
Pred. No. 5.06e-118;
0; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki, T. and Minobe, Y. Rice cDNA from callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Takuji Sasaki
Query Match 12.3%;
Best Local Similarity 67.3%;
Matches 410; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93758954
C96653.1 GI:3758954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poaceae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa.
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Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                        1 (bases 1 to 527)
Wemman, T., deButijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R90561 527 bp mRNA EST 30-DEC-1997 16916 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189H3T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 TATGTTTATCGGAGGATGTATAAGAATGGACAAGTAATACCGCTGGATGACTCCCTTGAT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TAIGCAGCAAACTTTTCACACATGCTTGGGTTTGATGATCCCAAAATGCTCGAGTTGATG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGGTGGAAATTTCGCACACATGTTGGAATTTGATAGCCCCCAGAAGCTTGAGCTGATG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGACTATATGTGACAATCCACACTGATCATGAAGGTGGAAATGTCAGTGCTCATACTGGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCTGGTTGGAAGTGCTCTGTCAGATCCTTATCTTTTTGCAGCTGCACTGAATGGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGCTGGACCATTGCACGCCTGGCTAATCAGGAAGTGCTGTTGTGGATCAAATCTGTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  802 TIGGCIGGGCCACTCCAIGGAITAGCCAACCAGGAAGICCIGCGGGGAITAAAICAGIT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 ATAGGTGAGACAGGTAGTGATGTTACAACTGATCAACTCAAAGAGTATGTGTGGGAAGACA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 862 GITGAIGAAIGIGGAGAAGAACAICICGACAGAGCAGITGAAAGAITAIGITIGGAAGACA 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TATGITIACCGGAGGATCTICAAGGATGGGAAAACTATAGCAGCTGATAATGCACTGGAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 CIAAAAAGGIGGAAAGGIIGTICCIGGCIC-GGICAIGGAGTICIACGIAAGACCGAI 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  742 CATTIGGIGGGIAGICCACTITCAGAICCTIAITIGICATTIGCAGCAGCATTAAAIGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.16e-115;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 188; DB 24;
                                                                                                                                                                                                                                                                                                                                                   118 t
                                                                                                                                                                                                                                                                              /map="11"
/clone="C10531_5A"
/clone_lib="Rice callus"
a 76 c 108 g 118
                                                                                                                                           /organism-"Oryza sativa"
               Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 73.1%;
305; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                               PROJECT = 'RGP'
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Japan 305
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AUTHORS
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KEYWORDS
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JOURNAL

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Strain—"var columbia"

/strain—"var columbia"
/note—"vercor: lambda zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dr primed cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 TCAGCAGATITACGAAAACGTGCITCIAICCCAGACCATGTGTACAAAAAAAAATGATGCT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 ATACCIGAAIGCCAGAAACTITIACCCGCIGCAAGIGCIGGIGCAGAGCCAIIGCCIGAA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 TCGAAAGACTTGGCGAACCGTGCTGCTGTGCCAGATTATGTGTACAATGCCATCGATGCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 CTGCCTTCCACAGCTCATCCAATGACTCAATTTGCTAGCGGTGTTATGGCCCTCCAGGTG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 CTACCTATTACGCCTCATCCAATGACTCAGTTTTGCACTGGTGTTATGGCCTTACAGACT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 CAAAGTGAGTTTCAAAAGGCATATGAGAATGGAATTCATAAGTCAAAGTTCTGGGAGCCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 ACATATGAGGATTGCCTCAACCTGATTTGCTCGTGTTNCCTGTTGTAGNCTGCATAATGT 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                               MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
95148729
On Apr 14, 1993 this sequence version replaced gi:693674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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0; Mismatches 80;
                                                                                                                                                                                                                                                                                                     /organism-"Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="873F09; 1q21.3-1q23.2; 9"/clone="189H3T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 31;
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                                                                                    MSU-DOE Plant Research Laboratory Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Lambda-PRL2"
106 c 122 q 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 183;
                                                                                                                                                 Lansing,Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"taxon:3702"
                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 TTATCCGAAGGGATGTATAANAAT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567 ITAICGGA--GGAIGIAIAAGAAI 588
                                                               Contact: Thomas Newman
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77.6%;
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Matches 298; Conservative
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AU002699
94159092
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1186 TITGGGGTATCAAGGAGTCTTGGAATATGCTCACAGCTTATATGGGACCGAGCTCTTGGC 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            946 GGATTTGGTCTAGGAGTATTGCGGAAGACAGATCCAAGATACACATGCCAAAGAGAATTT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GCTAATCAAGAGGTTCTGGTATGGCTCGAGAACTGCGCAAACAAGTTGGTGATAATTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ACAGAAGAGCAACTCAAAGAATTCATCTGGAAAACACTTAAATCTGGTCAGGTTGTACCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886 TCGACAGAGCAGTTGAAAGATTATGTTTGGAAGACACTAAACAGTGGCAAGGTTGTACCT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GGTTACGGTCATGCAGTACTTAGAAAACTGATCCAAGATATACTTGCCAGCGTGAGTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GCTCTTAAGCACTTACCCAATGACCCATTATTCAAGCTGGTCGCTGCTGTTTACAAGGTT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GTTCCGCCGATCCTCACCGAACTTGGCAAAGTCAAGAAGCCATGGCCTAATGTAGACTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 CATTCGGGAGTTCTTTTGCAGTATTATGGTCTGAAGGAGATGAACTACTATACAGTAATG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 TTTGGAGTGTCCCGAGCGTTGGGTGTTCTCGCTCAGTTGATTTGGTCCCGTGCGCTCGGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GATCCTTACTTATCTTTCGCGGCTGGACTCAATGGTCTTGCTGGACCACTTCACGGCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766 GATCCTTATTTGTCATTTGCAGCAGTAAATGGTTTGGCTGGGCCACTCCATGGATTA 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               706 GATCATGAGGGTGGAAATGTTAGTGCACACACTGGCCATTTGGTGGGTAGTCCACTTTCA 755
                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Lepidoptera; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACCACGAGGGTGGAAACGTTTCTGCGCACACTACGCATTTAGTGGGTTCTGCTTTAGT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 178; DB 26; Length 620;
Pred. No. 8.20e-108;
0; Mismatches 202; Indels 0;
                                                                                                                                                Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S. Establishment of cDNA database of Bombyx mori
                                                                                                                                                                                                    Unpublished (1999)
On Sep 1, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1246 TIGCCGCTAGAGAGCCAAAGAGTGTCACTATGGAATGGCTT 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Bombyx mori p50(Daizo)"
141 c 146 g 171 t
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                                                                                                                                                                                                                                                                        Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: Kmita@uexs64.nirs.go.jp
PROJECT = CREST Project by JST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="n0357"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 65.3%;
Matches 380; Conservative
                     domestic silkworm.
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ORIGIN
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JOURNAL
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KEYWORDS
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RESULT

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1 (Bases 1 to 501)
S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C.,
White, O., Sutton, G., Blake, J.A., Erandon, R.C., Man Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Philips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Billion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                      EST185581 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to citrate synthase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser, C.M. and Venter, J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.iigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843 GCTGTGGATTAAATCAGTTGTTGATGAATGTGGAGAGACATCTCGACAGAGCAGTTGAA 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="organ colon, Vector pBluescript SK', Site_1.
EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):109839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGCAGCAGCCATGAACGGGCTGGCAGGCCTCTCCCATGGACTGGCAAATCAGGAAGTGCT 60
19-APR-1997
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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/cell_line="KM12C(HCC)-parental human colon
carcinoma;Dukes B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.6%; Score 164; DB 11; Length 501; Best Local Similarity 66.9%; Pred. No. 7.09e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
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EST
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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
                                                                                                                                                      AA313713.1 GI:1966042
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501 bp
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AA313713
                                                                                                                  91966042
                                                                                                                                                                                                                       human.
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                          DEFINITION
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                                                                                           ACCESSION
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COMMENT
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes; Spermatophyta, Magnoliophyta; Liliopsida, Poales,
(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1070 CTCCTATTCTATTAGAGCTTGGAAAGGTAAAGAATCCATGGCCTAATGTTGATGTTGATGTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               950 TIGGICIAGGAGIATIGCGGAAGACAGATCCAAGATACACAIGCCAAAGAGAATITGCGI 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1130 GIGGAGITITICCIGAACCACIAIGGITIGACAGAAGCAAGAIACIATACGGITITIGITIG 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  890 CAGAGCAGTTGAAAGATTATGTTTGGAAGACACTAAAACAGTGGCAAGGTTGTACCTGGAT 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 TGAAACATCTGCCTAAGGATCCCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 CCAATATCCTCTTAGAGCAAGGGAAGGCTAAGAACCCTTGGCCCAACGTAGACGCTCACA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 GTGGGGTGCTGCTCCAGTACTATGGCATGACGGAGATGAACTACTACTACAGTCCTGTTTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 ACGGTCATGCAGTACTGAGGAAGACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         710 ATGAGGGTGGAAATGTTAGTGCACACACTGGCCATTTGGTGGGTAGTCGACTTTGAGATC 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 CTTACCTGTCCTTTGCAGCAGCCATGAATGGGCTGGCGGGGCT-CTACATGGACTAGCAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 CTTATTTGCATTTGCAGCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCA 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGGGTGGTAATGTAAGTGCCCACACACACATTTGGTGGG-AGCGCTGTT-CAGACC 58
                                                                                                                                                                                                                                                                                                                                                                                                     3; Caps
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VanDeynze, A.E., Sorrells, M.E., Park, W.D., Ayres, N.M., Fu, H.,
Cartinhour, S.W. and McCouch, S.R.
Anchor Probes for Comparative Mapping of Grass Genera
Onpubblished (1997)
On Nov 29, 1993 this sequence version replaced gi:634857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA231705
307 bp mRNA EST 27-FEB-199
CD0534.R cDNA from oat Avena sativa cDNA clone CD0534, mRNA sequence.
AA231705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AIGAGAAGITACGAGACIACAICIGGAACACACICAAITCAGGACGGGIGGICCCCAGGAI
                                                                                                                                                                                                                                                                                                                                              Length 522;
                                                                                                                                                                                                                                                                                                                                              Score 156; DB 10; Length 522
Pred. No. 1.17e-90;
0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1190 GGGIATCAAGGAGTCTTGGAATATGCTCACAGCTTATATGG 1230
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                                                                                                                                                        /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                   150 g
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AA231705.1 GI:1854091
                                                                                                                                                                                                                                                                                                                                              Query Match 10.1%;
Best Local Similarity 66.4%;
Matches 346; Conservative
                                                                                     Bonaldo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gassel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,N., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1143 GAACCACTATGSTITGACAGAAGCAAGAIACTAIACGTITGTITGTITGGGGTAICAAGGAG 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1082
                                                                                                                                                                                                                                           241 TAATGACCCCATGTTTAAGTTGGTTGCTCAGCTGTACAAGATTGTGCCCAATGTCCTCTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 CCAGTATTATGGCATGACGGAGATGAATTACTACACGGTCCTGTTTGGGGTGTCACGAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 ATTGGGTGTACTGGCACAGCTCATCTGGAGCCGAGCCTTAGGGTTCCCTCTAGAAAGGCC 480
                                 121 AGACTACATCTGGAACACACTCAACTCAGGACGGGTTGTTCCAGGCTATGGCCATGCAGT 180
                                                                                                                                    181 ACTAAGGAAGACTGATCCGCGATATACCTGTCAGCGAGAGTTTGCTCTGAAACACCTGCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
                                                                                                                                                                                                                                                                                                                                                                             903 AGATTATGTTTGGAAGACACTAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGGAGT
                                                                                                                                                                                   963 ATTGCGGAAGACAGATCCAAGATACACATGCCAAAGAGAATTTGCGTTGAAGCACTTGCC
                                                                                                                                                                                                                                                                                               1023 IGAIGACCCATITITICAATIGGIGICAAAGIIGIAIGAAGIGGAGCGIGCCICCIAIICIATI
                                                                                                                                                                                                                                                                                                                                              301 AGAGCAGGGTAAAGCCAAGAATCCTTGGCCCAATGTAGATGCTCACAGTGGGGGTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1392879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                 /note="Vector: Uni-ZAP XR/pBluescript; Site_1: EcoRI; Site_2: XhoI; A Uni-ZAP XR cDNA library was constructed from etiolated leaf mRNA from the oat cultivar 'Brooks' and converted to pBluescript (amp resistant) as described in Heun et al. (1991) Genome 34:437-447. For insert amplification, use M13 forward and reverse primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones from this library are designated with the prefix 'CDO'. *Note: Clone CDO1081 was recloned into the TA cloning vector and carries kanamycin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA112941 466 bp mRNA EST 01-AUG-1997 2D59066.rl Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562451 5' similar to SN:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                787 GCAGCATTAAATGGTTTGGCTGGGCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTG 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TACGTATGGAAGACACTGAAGAGTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CGTAATACAGATCCACGATACTCGTGCCAAAGGGAGTTTGCACTTAAGTATTTACCCCGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TGGATCAAATCTGTGATGGAAGAAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAA 120
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1 (bases 1 to 466)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Lew,, Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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9.7%; Score 151; DB 10; Length 307;
Local Similarity 75.8%; Pred. No. 8.76e-87;
hes 222; Conservative 0; Mismatches 71: Indels 1
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/clone_lib="cDNA from oat"
                                                                                                                                                                                                                                                                                        /organism="Avena sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="etiolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 9
                                                                                                                                                                                                                                                                                                             /cultivar="Brooks"
                                                                   Cornell University
Ithaca, NY 14853-1901, USA
Tel: 607 255 0420
Fax: 607 255 6683
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                                             Dept Plant Breeding
                      Contact: McCouch SR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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/note="Organ: skeletal muscle; Vector: pBluescript SK-; Ste_1: BooRs; Site_2: xhol; Cloned unidirectionally. Primer: Oligo dT. Skeletal muscle from patient with malignant hyperthermia. Average insert size: 1 0 kb; min_APA xR Vector; -5' adaptor sequence: 5' GAATTGGGCAGGG 3' -3' adaptor sequence: 5' CTGGAGTTTTTTTTTTTTTT 3'" /db_xref="GDB:4595741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vh38g11.rl Barstead mosepooled organs MPLR84 Mus musculus CDNA clone IMAGE:889316 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHAEE, MITOCHONDRIAL PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2292 std Error: 0.00 seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 AATTICACCAACAIGITAGGCIATACIGAICAICAGTICACIGAGCTCACGCGCCCTGIAC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 CTCACCATCCACAGIGACCATGAGGGTGGCAATGTAAGTGCCCATACCAGCCATTGGTG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 GGCAGTGCGTNTTCCGACCCGTTACCTGTCCTTTGCAGCAGCATGAACGGGCTGGCAGG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810 GCCACTCCATGGATTAGCCAACCAGGAAGTCCTGCTGTGGATTAAATCAGTTGTTGATGA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 AGTTGGCAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCTGGAACACACTCAACTC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 AATTTCGCACACATGTTGGGATTTGATAGCCCTCAGATGCTTGAGCTGATGCGTTTAT 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 TGGCAAGGTIGTACCTGGAITTGGTCTAGGAGTATTGCGGAAGACAGATCCAAGATACAC 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 127; Indels 3; Gaps
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                                                 Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:693136
                                                                                                                                                                                                               Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:562451"
/clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
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                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 143; DB 36;
Pred. No. 1.31e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 423.
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                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage-"adult"
WashU-Merck EST Project
Unpublished (1995)
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Best Local Similarity 68.8%;
Matches 287; Conservative
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                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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960 ACTATIGCGGAAGACAGAICCAAGAIACACAIGCCAAAGAGAAITIGCGIIGAAGCACII 1019
                                                                                                                                                           1020 GCCTGATGACCCATTTTTTCAATTGGTGTCAAAGTTGTATGAAGTGGTGCCTCCTATTCT 1079
                                                                                                                    381 GCCTAAAGATCCCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGCCCCAATATCCT 440
                                      321 AGTACTGAGGAAGACTGACCCTCGCTATTCCTGTCAGCGAGTTTGCTCTGAACATCT 380
900 GAAAGATTATGTTTGGAAGACACTAAACAGTGGCAAGGTTGTACCTGGATTTGGTCTAGG 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 t
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                                                                                                                                                                                                   441 CTIAGAGCACGGGAAGGCTAAGAACCCTIGGCC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 GIGGAGAAGAIAIAICAA-AGAACAGIIGAA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        872 GIGGAGAGAACAICICGACAGAGCAGIIGAA 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
/clone="TAT2B1"
/clone_lib="AC16H"
40 c 52 g
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Best Local Similarity 84.49;
Matches 178; Conservative
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UMR05 CNRS/INRA
                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
217455
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SOURCE
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                                                                                                              Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 473)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 TAATGTAAGTGC-CACACAAGCCATTTGGTGGGCAGCGC-CTTTCAGACCCTTACCTGTC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 CTTTGCAGCAGCATGAATGGGCTGGGGGGCT-CTACATGGACTAGCAATCAGGAGT 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 ACGAGACTACATCTGGAACACACTCAATTCAGGACGGGTGGT-CCAGGATACGGTCATGC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660 CCCTCAGATGCTTGAGCTGATGCGCCTTTATGTCACAATTCACAGTGATCATGAGGGTGG 719
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                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 GCTIGTCTGGCTGACACACCTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTT
                                                                                                                                                                                                                                                                              Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1402331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                            Washu'HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 9.2%; Score 143; DB 14; Length 473; Best Local Similarity 68.0%; Pred. No. 1.31e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
122 c 124 g 107 t
                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .473
/organism-"Mus musculus"
                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
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              4A498291.1 GI:2233314
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                                                                          Mus musculus
                                                           house mouse.
                                                                                                                                                                                                                                            Waterston, R.
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217455 213 bp mRNA EST 10-NOV-1992 ATTS0029 AC16H Arabidopsis thaliana cDNA clone TAT2B1 5' similar to CITRATE SYNTHASE, MITOCHONDFIAL PPECUFSOF. SWISS-Prot entry P00889,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/note="Vector: Lambda ZAPII; tissue=cell suspension
culture of ecotype columbia; clone_library=Acli6H; Cloning
vector: Lambda ZAPII; Physiological condition: cycling
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis. 1 (bases 1 to 213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Arabidopsis thaliana transcribed genome: the GDR cDNA program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 GTAGIGCACITICAGACCCATAICIGICATITIGCAGCIGCATIAAAIGGITTAGCIGGGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      752 GTAGTCCACTTTCAGATCCTTATTTGTCATTTGCAGCAGCATTAAATGGTTTGGCTGGGC 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
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BP 27,31338 Castanet-Tolosan cedex, France
Email: lescuredtoulouse.inra.fr.
Location/Qualifiers
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/organism-"Arabidopsis thaliana"
/strain-"var columbia"
/note-"voctor: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA lbrary derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Obiroge, J., Raikhel, N., Somerville, S., Thomashow, M., Setzel, E. and Somerville, C. Genes qalore: a summary of methods for accessing results from large scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 252)
                        AA720224 252 bp mRNA EST 30-DEC-1997
33417 Lambda-PRL2 Arabidopsis thaliana cDNA clone 158x12T7, mRNA
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MSU-DDE-PRL, Michigan State University,Plant Biology Bldg.,E.
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/clone_lib="Lambda-PRL2"
| 54 c 64 g 67
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
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Location/Qualifiers
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Arabidopsis thaliana
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RESULT 15
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1247 TGCCGCTAGAGAGGCCAAAGAG 1268
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Search completed: Sat Oct 23 19:13:43 1999 Job time: 2657 secs.

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Release	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
MPsrch_pp prote	protein - protein database search, using Smith-Waterman algorithm
Run on: Tabular output no	Fri Oct 22 15:45:02 1999; MasPar time 17.45 Seconds 532.612 Million cell updates/sec
ion: Score:	15-08-702-718-4 437) from USO8702718.pep
Sequence:	A SONDOBYSCHAZOVER LERYNSVIRBNDERFURRR 43/PPM 150
Searched:	Gap 11 170751 segs, 21266608 residues
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	a-geneseq35 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 39:part29 30:part30 31-part31 37:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 35.586, Variance 154.962; scale 0.230

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	& Query Match	Query Match Length	DB	ID	Description	Pred. No.
	3243	100.0	437	14	R82839	Sugar beet citrate sy	3,53e-302
Cŧ	2800	86.3	469	14	R82840	Tobacco citrate synth	1.87e-258
m	2637	81.3	471	15	R86383	Potato citrate syntha	2.20e-242
4	2637	81.3	471	14	R82838	Potato citrate syntha	2.20e-242
S	312	9.6	436	m	R14357	Citrate synthase enco	4.10e-17
9	103	е С	657	53	W20051	Methionyl-tRNA synthe	1.28e+01
7	101	3.1	456	34	W38570	Methyl tetrahydropter	1.77e+01
œ	66	3.1	266	39	W87531	An antitumour protein	2.45e+01
6	100	3.1	738	31	W56163	New DNA sequence isol	2.08e+01
10	93	2.9	219	17	R89749	AFT-1 interacting pro	6.36e+01
11	94	2.9	237	21	W20183	H. pylori cell envelo	5.44e+01
12	93	2.9	324	15	R84104	Equine herpesvirus (E	6.36e+01
13	93	2.9	324	σ	R52668	Equine herpesvirus US	6.36e+01
14	95	2.9	329	59	W55574	H. pylori ORF 06ep302	4.64e+01
15	95	ر د	329	σ. Ci	W55330	H. pylori ORF hp3e110	4.64e+01
16	94	6.0	461	C1	W21009	H. pylori cell envelo	5.44e+01

61 eegirfrgfsipecgkllpaasagaeplpegllwllltgkvpskeqvdalsadlrkrasi 120

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Partial sequence of b 6.36e+01 Omega-cyclohexane fat 6.36e+01 Cellulose synthase op 6.36e+01 Human secreted protei 1.02e+02 Human secreted protei 1.02e+02 Rat CC Cómoxhine rece 1.02e+02 Staphylococcus aureus 7.44e+01 Class II EPSP synthas 7.44e+01 Cystathionine gamma s 1.02e+02 NTH1 HxuB protein. 8.70e+02 NTH1 HxuB protein. 8.70e+01 Lactobachlius amylovo 8.70e+02 Peptide derived from 1.88e+02 Chimeric anti HIV ant 1.88e+02 Chimeric anti HIV ant 1.88e+02 Tyrosine phenollyase 1.61e+02 Sequence transcribed 1.61e+02 Sequence transcribed 1.61e+02 Peptide Bo-1 Carboxydothermus hydr 1.88e+02 Peptide Bo-1 Carboxydothermus hydr 1.88e+02 Carboxydothermus hydr 1.88e+02 Carboxydothermus hydr 1.86e+02 CF-5 pathogen resista 1.61e+02 CF-5 Pathogen resista 1.61e+02 Tytorlone gene cluste 1.19e+02 Tytorlone persista 1.61e+02 CF-5 Pathogen resista 1.61e+02 CF-5 Pathogen resista 1.38e+02 Virulence gene cluste 1.19e+02	rrober B, Landschuetz.  used to regulate flown to reduce sprouting h. from sugar beet was produced using radioactive D blanum tuberosum citrate tabacum citrate synthas sequenced. The nt. sequenced.	3243; DB 14; Length 437; No. 3.53e-302; Ismatches 0; Indels 0; Gaps 0; sfqlgninvdmvlggmrgmtgllwetslldp 60
R79163 WA71636 WA71636 WA746000 WA74904 WA7490173 WA71618 WA7164 WA716 WA7164 W	ALIGNME  437 AA.  e. linie 5S  GREVO GM  V, Mull  synthas  rs, etc.  synthas  rs, etc.  pp; Engli  gar beet  gar beet  xture of  xture of  Nicotia	0%; Score 3 0%; Pred. N ve 0; Mi erlkkikkefgs 
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DNA encoding plant citrate synthase - used to regulate flower formation,
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                                   121 pdhvyktidalpitahpmtqfctgvmalqtrsefqkayekgihkskfweptyedclslia
                                                                                                                 181 qvpvvaayvyrrmykngqviplddsldyggnfahmlgfdspqmlelmrlyvtihsdhegg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 60-63; 87pp; English.

To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solanum tuberosum citrate synthase cDNA (T04199). One of the clones was sequenced, The nt. sequence is
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larity 85.7%; Pred. No. 1.87e-258;
Conservative 34; Mismatches 27; Indels :
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Citrate synthase; flower formation.
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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Talso new CS sense and anti-sense DNA sequences

Claim 5: Page 15-19: 35pp; German.

The potato citrate synthase (CS) gene or cDNA sequence encoding CS (T03410) may be used to produce antisense CS sequences. CS DNA sequences are useful for altering CS activity in plants. Antisense CS sequences can be used to inhibit CS expression in plants and has the effect of inhibiting flower formation and by doing so improves the plant's storage capacity. This is partie, useful in crop plants of any kind but esp. useful in potatoes. In addition to altering CS activity the DNA sequences can also be used to identify similar sequences in the genomes of other plants and in the production of transgenic plants with altered CS activity. This sequence

represents the anino acid sequence of potato citrate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PEEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWILLITGKVPSKFQVDALSADI,RKFAS 119
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                                                                                                                                                                                                                                                                                                                                                                   301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 ssgldlrselvqelipeqqdrlkkiksdmkg-signitvdmvlggmrqmtgllwkphyld 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                   nvsahtghlvasalsdpylsfaaalnglagplhglangevllwiksvveecgeniskegl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Citrate synthase; inhibitor; increased storage capacity; potato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Landschutze V, Muller-Roeber B, Landschuetze V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2637; DB 15;
Pred. No. 2.20e-242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R86383 standard; Protein; 471 AA.
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Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 pksvtmewlenhckk 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 PKSVTMEWLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potato citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-1994; DE-408629.
22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanum tuberosum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antisense DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R86383;
                                      181
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JT 6
W20051 standard; Protein; 657
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Best Local Similarity 31.1%;
Matches 102; Conservative
                                                                                                                                                      453 lerpksvtmewlengckk 470
                                                                                                                                                                                     418 LERPKSVTMEWLEKFCKR 435
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                                                                                                                                                                                                                                                                                                                                                                                                                   (NAKA-) NAKANO SUMISE KK.
WPI; 91-329112/45.
                                                                                                                                                                                                                                                                                                             Acetic acid resistance.
                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-1989; JP-033776.
05-FEB-1990; JP-024395.
                                                                                                                                                                                                                                                                                                                                                        27-SEP-1991.
05-FEB-1990; 024395.
                                                                                                                                                                                                                                                                                                                           Acetobacter sp. J03219878-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting Disclosure; Page 53-50 Ppp; English.

To identify a cDNA from potato which codes for citrate synthase, a CDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A. thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of introduce BamHI cleavage sites at both ends of the amplified cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. The nt sequence is given in T04199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 iaqvplvaayvyrrmykngdtipkdesldyganfahmlgfsssemhellmrlyvtihsdh 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eggnvsahtghlvasalsdpylsfaaalnglagplhglangevllwiksvveecgenisk 333
                              274 eggnvsahtghlvasalsdpylsfaaalnglagplhglangevllwiksvveecgenisk 333
                                                                                                                                                                                   358 PILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 pdegirfrglsipecqkvlpaakpggeplpegllwllltgkvpskeqvnsivsgiaesgi 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 IPDHV-YKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSL 178
                                                                                                                       298 EQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 ssgldlrselvqelipeqqdrlkkiksdmkg-signitvdmvlggmrgmtgllwkphyld 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
179 IAQVPVVAAYVYPPMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLEL-MRLYVTIHSDH
                                                eqlkdyvwktlnsgkvvpgfghgvlrktvprytcqrefamkhlpedplfqlvsklyevfl
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                                                                                                                                                      lflgnlaklk-pwpnvdahsgvllnyygltearyytvlfgvsralgicsgliwdralglp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 La Cognata U, Landschutze V, Muller-rober B, Landschuetze V;
Mueller-roeber B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                       Potato citrate synthase.
Citrate synthase; flower formation; tuber storage.
Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.3%; Score 2637; DB 14;
Best Local Similarity 81.3%; Pred. No. 2.20e-242;
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                                                                                                                                                                                                                                                                                              T 4
R82838 standard; Protein; 471
                                                                                                                                                                                                                  453 lerpksvtmewlengckk 470
                                                                                                                                                                                                                                               418 LERPKSVTMEWLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                        25-JAN-1996 (first entry)
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22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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N-PSDB; T04199.
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Score 312; DB 3; Length 436;
Pred. No. 4.10e-17;
85; Mismatches 108; Indels 33; Gaps 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 vyknfdprakimgqtchevltelgikddplldlavel-ekia-lsddyfvgrklypnvdf 372
                                                                                                               91 eeviylllngelpnkaqydtftntltnhtllheqirnffngfrrdahpmailcgtvgals 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 VLRKTDPRYTC-QRE-FA-LKHLP--DDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDA 375
                                                                     334 eqlkdyvwktlnsgkvvpgfghgvlrktvprytcqrefamkhlpedplfglvsklyevfl 393
238 EGGNVSAHTGHLVGSFLSDFYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENIST 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetic acid resistant gene with in plasmid and transformed acetobacter - improves yield of acetic acid fermentation. Disclosurer, Fig 5: 12pp; Japaneses.

The arrA gene encodes the citrate synthase and is part of an acetic acid resistance operon comprising aarA, aarB and aarC. The DNA can be used to prepare an acetic acid resistant strain of bacteria for use in acetic acid fermentation.
                                                                                                                                                                                                                  394 Iflgnlaklk-pwpnvdahsgvllnyygltearyytvlfgvsralgicsgliwdralglp
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R14357 standard; Protein; 436 AA.
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Citrate synthase encoded by aarA.
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Matches
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                                                                                                                                                                                                              DNA encoding methionyl-tRNA synthetase from Staphylococcus aureus word 29 - useful for protection against bacterial infections and collaim 1. Pages 19-20. 3 ppp. English.

WCUH 29 - useful for protection against bacterial infections action in the present sequence is a novel methionyl tRNA synthetase protein from Staphylococcus aureus strain WCUH29 (NCIMB 40771), which is related by amino acid sequence homology to Bacillus subtilis tRNA synthetase encoded by the mets gene. The enzyme catalyses the aminoacylation of tRNA-Met, by a two step mechanism. The first step involves formation of a stable enzyme.methionyl adenylate complex resulting from the specific binding and reaction of ATP and L-methionine. Subsequently, the 3' terminal adenosine of anyme-bound tRNA-Met reacts with the aminoacyl adenylate, leading to the seterification of the tRNA and release of AMP. Vectors comprising the DNA (or polynucleotides having at least 70 % identity to it) can be used for the recombinant production of the animonological response in a mammal to generate antibodies to protect against disease. The antibodies protect against disease. The antibodies protect against disease. The antibodies protect against invasion of bacteria, e.g. by blocking adherence of bacteria to damaged tissue, including wounds in skin or connective insummantation of in-dwelling devices, or wounds in the mucous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methyl tetrahydropteroyltriglutamate-homocysteine methyltransferase. Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound; pathogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Methionyl-tRNA synthetase from Staph. aureus.
tRNA synthetase: Bacilius subtilis; mets; immunological response; antibody; bacterial infection; adherence; damaged tissue; wound healing; skin; protection; vaccine.
Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23; Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MXY-1997; U07950.
14-MAY-1996; US-017670.
(SMIK ) SMITHKLINE BEEGRAM CORP.
(SMIX ) SMITHKLINE BEEGRAM PLC.
Black MI, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 ilmkdgkmskskgnv-vdpnilidrygldatryy 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Pages 342-344; 483pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 103;
Pred. No. 1
                                                                                         23-JUL-1997.
17-JAN-1997. 300317.
19-JAN-1996. GB-001095.
27-JUL-1996. GB-015445.
(SMIK ) SMITHKLINE BEECHAM PLC.
Hodgson JE_Lawlor EJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W38570 standard; Protein; 456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 3.2%;
Local Similarity 38.2%;
les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae.
                                                                                                                                                                       son JE, Lawlor EJ;
97-365943/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 98-008793/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              657 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T98621.
                                                                                                                                                                                                      N-PSDB; T71309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membranes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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This sequence represents a Streptococcus pneumoniae protein that, based on homology with an E. coll protein, is a methyl tetrahydropteroyltri glutamate-homocysteine methyltransferase, and is encoded by a DNA of the invention. The DNA sequences were isolated from S. pneumoniae strain closops (NCIME 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or recall immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal propertion of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 vyadlvnlpvdaig1-dfvegkktlelvkggfpadktlyvgivngkniwrnnyekslavl 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 eqipa-enivltsscsllhv-pfttaneefepallnhfaf-avekldeirdldairnggg 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 dgyddsirgivvketlggtldasrgvttlplgverrtdnpiyvtwtgadtvlgdvpkspr 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches 65; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformed by vector containing base coding sequence Claim 1; Page 7-8; 15pp; Japanese.
The present sequence encodes an antitumour protein, and is isolated from Tricholoma matsutake.
Sequence 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 34; Length 456; Pred. No. 1.77e+01;
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15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An anti-tumour protein - prepared by culture of host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 sealaankelfatervqen-aelrariaq1tda 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 GGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGP 271
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Tricholoma matsutake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOMO-) MOMOYA KK.
(NOKO-) NORINSUISANSHO SHOKUHIN SOCO.
WPPI: 99-074153/07.
N-PSDB; V83626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W87531 standard; Protein; 566 AA
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Local Similarity 32.38;
Local Similarity 32.38;
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 19.6%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999 (first entry)
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13-FEB-1997; JP-029275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An antitumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 falvt 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CDNA and e.g. vector, host cell and polypeptide - used to produce polypeptide in high yields, which is used in cosmetics claim 9; pages 9-11. 15pp: Japanese. The present sequence represents protein encoded by a new DNA sequence isolated from Pinctada fucata. The protein be used as an ingredient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transduction events involved in plant defence responses to pathogens such as fungi, nematodes, bacteria and viruses.
Sequence 219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant transcriptional activator AFT-1 - isolated from Arabidopsis and useful for modifying gene expression and modulating plant defence responses to pathogens.

Bisclosure: Page 25-26; 4/Pp: English.

R89749 is a partial Arabidopsis proteasome, a plant defence-related protein (PRP). This protein and other PDRPS were isolated using a protein residues 33-194 fusion protein, i.e. AFTI (Arabidopsis 14-3-31) protein residues 33-194 fused to Lexa, a DNA binding protein, in an interaction trap assay. AFTI is a transcriptional activator protein and may be used to enhance, control or modify plant gene expression, e.g. in the regulation of plant storage components (esp. napin, legumin or phaseolin). AFTI can also be used to modulate signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFT-1 interacting protein (partial proteasome).

Arabidopsis fourteen-three-three 1, AFT1; Cruciferae; regulation; transcription activator; gene expression modulator; crucifer; signal transduction; defence response; gene therapy; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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Pred. No. 6.36e+01;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches 11; Indels
                                                                                                                      New DNA sequence isolated from Pinctada fucata.
Pinctada fucata; protein; cosmetic.
Pinctada fucata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.08e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 VIPLDDSLDYGGNFAHMLGFDSPQMLELMRLY 230
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22-JUN-1995; 109669.
23-JUN-1994; US-266451.
(CEHO ) GEN HOSPITAL CORP.
(MASS-) MASSACHUSEITS GEN HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R89749 standard; Protein; 219 AA.
                           W56163 standard; Protein; 738 AA
                                                                                                                                                                                                                                                                                    28-MXY-1997; 138461.
15-UUL-1996; JP-184459.
(MIKI-) MIKIMOTO SEIYAKU KK.
WPI; 98-254410/23.
N-PSDB; V22683.
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Local Similarity 45.2%;
Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 34.4%;
nes 11; Conservative
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                                                                                       28-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 AA;
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N-PSDB; I11341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis sp.
EP-693554-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cosmetics
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                                                                                                                                                                                                                                                               31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                              W56163;
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RESULT
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                           ID DATE DATE OF THE PART OF TH
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08-JUL-1997 (first entry)
18. pylori cell envelope transporter protein, 179677.aa.
Cytoplasmic; vaccine; prevention; treatment; infection; identification;
Cytoplasmic; vaccine; prevention; life cytole; activator; bacteria; inhibitor;
duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 30; rages 401; Habitobacter pylori cell envelope transporter protein. The protein may be used in a vaccine to prevent or treat Protein. The protein may be used in a vaccine to prevent or treat P. Dylori infection or to identify H. Pylori polypeptide binding compounds, useful as potential H. Pylori life cycle activators or inhibitors. The genomic sequence of H. Pylori (ArCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. Pylori antigens for vaccine development, the amilro acid sequences predicted from various ONF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 VVAAYVYRRMYKNGQVIPLD-DSLDYGGNFAHMLGFDSPQMLELMRLY--VTIHSDHEGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 viptfalalmptfndlvgfgvdsmgltpknahylgyiapvflvlvricqgvavggelpga 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1996 (first entry)
Equine herpesvirus (EHV4) unique short (US2) gene prod..
Equine herpesvirus 4; EHV4; unique short; US2; recombinant; vaccine; attenuated virus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related bolypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter Claim 56; Pages 401; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123..140
/note= "EHV-1, EHV-4, HSV-1, PRV, HSV-2, MDV, and
IBR consereved US2 region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 wvfvh-ehapqgq-kntyigflta-svvsgillgslvyigiymvfdkpvved 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 94; DB 21; Length 237;
24.1%; Pred. No. 5.44e+01;
Ative 33; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                        /note= "encoded by cocon GTR"
                                                                                                                                                                                                                                               'note- "encoded by codon TTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith D, Mellgaerd BL;
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                                                                                                                                                                                                       Location/Qualifiers
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R84104;
T 11
W20183 standard; protein; 237 AA.
                                                                                                                                                                cell envelope; transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 24.1%;
nes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                 06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Equine herpesvirus 4
                                                                                                                                                                                   Helicobacter pylori.
                                                                                                                                                                                                                           misc_difference 126
                                                                                                                                                                                                                                                                  misc_difference 127
                                                                                                                                                                                                                                                                                                                                                                                                                                     Berglindh OT, Smit
WPI; 97-052306/05.
N-PSDB; T67415.
                                                                                                                                                                                                                                                                                                                                                                                                                   (ASTR ) ASTRA AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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9
                                                                                                                                                                                                                                                     T00532 encodes R84104 the eqfine herpesvirus 4 (EHV) unique short 2 (US2) gene prod. A recombinant attenuated EHV can be produced by deleting the above US2 gene (a region not essential for replication) from the viral DNA. The attenuated virus can be used as a foetal safe vaccine to protect an equine against EHV, or in a test to determine if an equine has been vaccinated against or is infected with EHV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 nkswqpsfv-cgklfetiplttv-dykhllkq-kvlpgqdhpesarsllqhkssfvsppp 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nkswqpsfv-cgklfetiplttv-dykhllkq-kvlpgqdhpesarsllqhkssfvsppp 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 SKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNF-AHMLGFDSPQM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant equine herpesylrus' (EHV) have a foreign DNA sequence inserted into their genomes. The inserted sequence is a piece of foreign, double stranded DNA which encodes an RNA molecule which does not naturally occur in the animal into which the EHV is introduced. The foreign DNA sequence is introduced into the EHV is a homology vector. The recombinant EHV's are used to prepare vaccines to protect horses from infectious EHV. Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-1994 (first entry)
Equine herpesvirus US2 gene product.
Equine herpesvirus, US2; vaccine; antigen; protection; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equine herpesvirus (Strain: Dutta; Individual isolate: S-4EHV-000).
                                                                                                                                                     Recombinant equine herpes viruses pref. contg. a deletion in a region not essential for replication - used in vaccines to protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant equine herpes viruses - used to prepare vaccines to protect horses from infectious equine herpes virus Example 1; Paye 84-86; 153pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB 15; Length 324;
Pred. No. 6.36e+01;
24; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attenuated EHV's can be produced by removing the US2 gene. Sequence 324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 324;
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Pred. No. 6.36e+01;
                                                                                                                                                                                                         horses from infection
Example 13; Pages 89-90; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R52668 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.9%;
Local Similarity 24.7%;
Les 18; Conservative
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Best Local Similarity 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
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07-AUG-1992; US-926784.
16-FEB-1995; U02087.
17-FEB-1994; US-198094.
                                                                            Cochran MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 LELMRU-YVTIHS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 -nfkrliyavvdp 224
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                                           (SYTR ) SYNTRO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYTP ) SYNTPO COPP.
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                                                                                               95-302714/39.
                                                                                                                                                                                                                                                                                                                                                                                                                   324 AA;
                                                                                                                                N-PSDB; T00532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q56617
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                                                                         Chiang CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09403628-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Polypeptide(s) - useful in vaccines to treat or prevent H. pylori polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection
Claims 14,96; Page 779-779; 1145pp; English.
Claims 14,96; Page 779-779; 1145pp; English.
Claims 14,96; Page 779-779; 1145pp; English.
Cometabolism. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can discribution of H. pylori-specific antigens. The genomic sequence of ad distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 5679) was determined from overlapping contigg generated for ORF of at least 180 nucleotides, and the predicted coding regions for ORF of a least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF interest marriang the and determined from or exported interest particular marriance and determined from the requences of interest marriang the marriance and determined from the requences of interest marriang the marriance proteins. Having identified and determined the sequences of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
identification; binding compound; bacteria; life cycle; activator;
inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
Helicobacter pylori.
                                                         24-JUN-1998 (first entry)
H. pylori ORF O6ep30223_23557202_c2_130 cytoplasmic protein.
H. pylori orF of the prevention; treatment, infection; envelope: identification; binding compound bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 95; DB 29; Length 329;
Pred. No. 4.64e+01;
16; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 IAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAH 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W55330 standard; Protein; 329 AA.
W55574 standard; Protein; 329 AA
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Best Local Similarity 27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                   09-OCT-1997.

05-DEC-1997.

06-DEC-1996. US-761318.

29-MAR-1996. US-625811.

20-APR-1996. US-758731.

25-OCT-1996. US-738659.

28-OCT-1996. US-738859.

AMSTRA AB.

ALIM RA, SMITH DF.

WPI: 97-503122/46.
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US-625811.
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US-738859.
                                                                                                                                                                                                                         Helicobacter pylori.
WO9737044-Al.
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09-OCT-1997.
27-MAR-1997; U05223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V24983
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28-OCT-1996;
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                              W55574;
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DR (ASTRA AB.)

PT (ASTRA AB.)

DR (ASTRA AB.

C (ASTRA AB.)

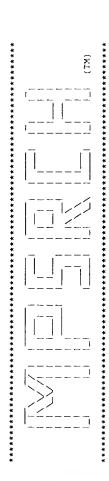
DR (ASTRA AB.)

C (ASTRA AB.
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Search completed: Fri Oct 22 16:48:53 1999 Job time : 231 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:32:52 1999; MasPar time 29.50 Seconds 871.352 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-2 (1-471) from USO8702718.pep 3466 1 MVFYPSVSLLSKLPSPAVQQ......PLERPKSVTMEWLENOCKKA 471 Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 49.897; Variance 94.480; scale 0.528 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
		مین					
Result		Query			;		
. ON	score	Match	Length	DB	ID	Description	Pred. No.
П	3466	100.0	471	10	043175	ETHANOLAMINE AMMONIA-L	L 0.00e+00
7	3098	89.4	469	10	024135	CITRATE SYNTHASE (EC	4 0.00e+00
3	2892	83.4	472	10	080433	CITRATE SYNTHASE (EC	4 0.00e+00
4	2820	81.4	474	10	C64869	CITRATE SYNTHASE (EC	4 0.00e+00
S	2637	76.1	437	10	096544	CITRATE (SI)-SYNTHASE	0.000+00
9	2058	7.000	339	10	024259	CITRATE (SI)-SYNTHASE	0
7	1897	54.7	466	4	075390	CITRATE SYNTHASE (EC 4	4 0.
8	270	7.8	411	7	053115	CITRATE SYNTHASE (FRAG	G 2.16e-28
6	264	7.6	411	C1	059777	CITRATE SYNTHASE (EC	4 2.91e-2
10	263	7.6	411	~	P77936	CITRATE SYNTHASE (EC	4 4.490-2
11	261	•	356	C a	054382		4 1.07e-2
12	251	7.5	372	Н	028929	CITRATE SYNTHASE (CITE	2 1.070-2
13	260	7.5	411	C1	060047	CITRATE SYNTHASE (EC	4 1.64e-2
14	259		411	C	059469	CITRATE SYNTHASE (EC	4 2.53e-26
15	258	7.4	411	~	059779	CITRATE SYNTHASE (EC	4 3.89e-2
16	256	7 . 4	411	C1	059775	CITRATE SYNTHASE (EC	4 9.20e-2
17	246	7.1	379	CI	034002	CITRATE SYNTHASE.	6.648.2
18	243	7.0	410	C1	059769	CITRATE SYNTHASE (EC	4 2.38e-2
19	523	9.9	379	<b>.</b> →	032705	CITRATE SYNTHASE (EC	4 8.73e-2
20	229	9.9	429	C a	033915	CITRATE SYNTHASE (EC	4 8.73e-2

.07e-1	5.60e-19	e-1	٣.	2.17e-14	٥.	.34e-1	2.46e-12	.466-1	2.466-12	3.63e-12	9.80e-08	6.30e-04	7.95e-02	2.00e-01			2.70e-01	3.65e-01	3.65e-01	3.65e-01	8.91e-01	۲.	1.60e+00	2.13e+00
CITRATE SYNTHASE (EC 4	CITRATE SYNTHASE (EC 4	-	CITRATE SYNTHASE (EC 4	E SYNTHASE (	CITRATE SYNTHASE (EC 4	CITRATE SYNTHASE (EC 4	CELLULOSE SYNTHASE SUB	CITRATE SYNTHASE (FRAG	SIMILARITY TO SOPA ECO	BIOTIN SYNTHETASE.	DNA FOR 3-KETOACYL-COA	REVERSE TRANSCRIPTASE.	RIBOSOMAL MATURASE.	T4C15.22 PROTEIN.	MYOBLAST CITY.	N5 METHYLTETRAHYDROMET	RIBOSOMAL MATURASE.	RIBOSOMAL MATURASE.	TRAW.					
068883	P94325	306	5923	σ	960	782	059235	23	059234	00	39	082859	10	057513	7.1	96	375	715	082180	016103	96	047160	062977	032540
~	C a	<b>C</b> 4	7	7	7	7	~	(4	C 1	C	~	~	7	7	7	4	7	۵	10	S	Н	œ	œ	C1
427	434	431	~	321	4	Н	Н	- 1	319	σ	6	S	σ	$\circ$	3	$\leftarrow$	480	0	1339	97	71	206	$\circ$	210
6.4		6.2				•	•				•		•	3.2		•	•	٠					3.0	
223	513	214	200	193	189	187	181	191	181	180	153	128	113	110	106	109	109	108	108	108	105	104	103	102
21	;; ;;	23	24	25	26	27	82	53	30	31	32	33	34	35	36	37	38	39	4.0	41	42	43	44	45

# ALIGNMENTS

RESULT 1 PRELIMINARY; PRT; 471 AA. 1D 043175; PRELIMINARY; PRT; 471 AA. AC 043175;		OS SOLANIM TUBEROSIM (POTATO).  OC EUKAPYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBPYOPHYTA; TRACHEOPHYTA;  OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS;  OC ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.	RP SEQUENCE FROM N.A.  RY SEQUENCE FROM STREE;  BY MENTINE OF 0602321	• • •	RL PLANTA 196:756-764(1995). CC -1- CATALYTIC ACTIVITY: ETHANOLAMINE - ACETALDEHYDE + NH(3). CC -1- COFACTOR: COBALMIN. DR EMBL; X75082; G483510;  DR PFAM; PF00285; citrate_synt; 1.	DR MENDEL; 15200; SOLtu:2977;mn15200. KW LYASE. SQ SEQUENCE 471 AA; 52612 MW; BC96A65C CRC32;	Query Match 100.0%; Score 3466; DB 10; Length 471; Rest Local Similarity 100.0%; Pred No 0.00+00; Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps	Db 1 MVFYRSVSLLSKLRSPAVQQSNVSNSVPWLQVQTSSGLDLRSELVQELJPEQQDPLKKIK 60	DE 61 SDMKGSIGNITVDMVLGGMPGMTGLLWRPHYLDPDEGIFFFGLSIPECQKVLPAAKPGGE 120	Db 121 PLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTGFATGV 180
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181 MALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDES 240

DP

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240
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                                                       241 LDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                           241 LDYGANFAHMLGFSSSEMHELLMRLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAA 300
                                                                                                                               301 LNGLAGPLHGLANQEVLLWIKSVVEECGENISKEOLKDYVWKTLNSGKVVPGFGHGVLRK 360
                                                                                                                                                                                                         361 TVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLNYYG 420
                                                                                                                                                                                                                                             361 TVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLINYYG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDM-KGSIGNITVDMVLGGMRGMTGLLWKFHYLDFDEGIRFRGLSIFECQKVLFAAKFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 VMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLDYGANFAHMLGFSSSDMHEL-MKLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVFYRSVSLLSKLRSRAVQOSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVFYRGVSLLSKLRSRAVQOTNLSNSVRWLQVQTSSGLDLRSEL-QELIPEQQDRLKKLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.
                                                                                                                                                   181 MALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EPLPEGLLWLLITGKVPSKEQVDSLSQELRSRATVPDHV-YKTIDALPVTAHPMTQFATG
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4
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LA CGONATA U. LANDSCHUETZE V., WILLMITZER L., MUELLER-POEREP
PLANT CELL PHYSIOL, 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.4%; Score 3098; DB 10; Length 469;
                                                                                                                                                                                                                                                                                   421 LTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                469 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X84225; E13432; --
PROSITE; PSOOMBO; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
SEQUENCE 469 AA; 52492 MW; 6BE3G32;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL. 05, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITI.
NICOTIANA TABACUM (COMMON TOBACCO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITRATE SYNTHASE (EC 4 1 3 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 89.68;
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                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 RKTVPRYTCQREFAMKHLPPEDPLFQLVSKLYEVFLLFLQNLAKLK-PWPNVDAHSGVLLN 417
298 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                           300 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLR 359
                                                                                 358 KIDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 KAEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPEEGIRFRGLSIPECQKLLPGAKPG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 GEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 GVMALQVQSEFQKAYEKGIHKTKYWEPTYEDSITLIAQLPVVAAYIYRRMYKNGQSISTD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 DSLDYGANFAHMLGYDSPSMQEL-MRLYVTIHTDHEGGNVSAHTGHLVASALSDPYLSFA 2977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAJCUS CAROTA (CARROT).
SUKRAYOTA, VIREDIELANTAE: STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPREWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE: ARALIALES; APIACEAE: DAUCUS.
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                                                                                                                                                                       418 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                            420 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTWEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O OXALOACETATE.
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55; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. MS YONSUN;
TAKITA E., KOYAMA H., SHIRANO Y., SHIBATA D., HARA T.;
"CDMA encoding carrot mitochondrial citrate synthase.";
SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
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EMBL; AB017159; D1033521; --
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PTACE; TRICARBOXYLIC ACID CYCLE.
SEQUENCE 472 AA; 52656 MW; D46C38CC CRC32;
                                                                                                                                                                                                                                                                                                      472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.48;
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Matches 383; Conservative
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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01-NOV-1998
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                                                                                                                                                                                                                                                                      EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AEPLPEGLIMILLITGKVPSKEQVEALSKDLANRAAVPDYV-YNAIDALPSTAHPMTQFAS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 GVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 ESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLUNASALSDPYLSFA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 AALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKILNSGKVV>GFGHGVL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 KSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEGIRFRGLSIPEC2KVLPTAQSG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 GVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARVPVVAAYVYRRMYKNGDSIPSD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 RNTDPRYVCOREFALKHLPDDPLFQLVSKLYEVVPPVLTELGKVKNPWPNVDAHSGVLLN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVFFRSVSAFTRLRSRVQGQSSLSNSVRWIQMQSSTDLDLKSQL-QELIPEQQDRLKKL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVFYRSVSLLSKLRSRA-VQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 KSLDYGANFSHMLGFDDEKVKEL-MRLYITIHSDHEGGNVSAHTGHLVGSALSDPYLSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 AALNGLAGPLHGLANQEVLLMIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYGHGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 HYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLALERPKSVTMDWLEAHCKXA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 YYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KADL S., MASON T.M., KEPLAVAGE A.P., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
  418 HYGLTEARYYTVLFGVSRAIGICSQLVWDRALGLPLERPKSVTMEWLENHCKKS 471
                      418 YYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY CITPATE + COA = ACETYL-COA + H(2)9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Mismatches 38; Indels
                                                                                                                                                                      (TREMBLREL. 07, LAST SEQUENCE UPDATE) (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2820; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- SIMILARITY TO CHEEP CITPATE SYNTHASES.
EMBL: ACO04521; G3128180; ---
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
PROSITE; ROAGEOUS CALLE ACOUNTY ACOUNTY ACOUNTY CALLE.
SEQUENCE 474 AA; 52782 MW; 64FF2AC6 CRC32;
                                                                                                                474 AA
                                                                                                                                                                                                                                                    ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)
                                                                                                                                                                                                                                                                                                               CAPPARALES; BRASSICACEAE; ARABIDOPSIS
                                                                                                                                                     01-AUG-1998 (TREMBLREL. 07, CREATED)
                                                                                                              PPT;
                                                                                                                                                                                                               CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 81.4%;
Best Local Similarity 79.1%;
Matches 375; Conservative
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OXALOACETATE
                                                                                                                                                                          01-AUG-1998
                                                                                                                                                                                        01-AUG-1998
                                                                                              T 4
064869
                                                                                                                                   064869;
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S.
                                  01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
(CITRATE (SI)-SYNTHASE (EC. 4.1.3.7) (CONDENSING ENZYME)
(CITRATE CONDENSING ENZYME) (CITPOGENASE) (CXALOACETATE TPANSACETASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 IAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMIGFSSSEMHELLMRLYVTIHSDH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 LFLQNLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PEEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 PDEGIRFRGLSIPECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVNSIVSGIAESGI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 ISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENIST 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 EGGNVSAHIGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 EQLKDYVWKILNSGKVVPGFGLGVLRKIDPRYTCQREFALKHLPDDPFFQLVSKLYEVVP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 EQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 PILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSPSLGIGSQLIWDRALGLP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSNLDLRSEL-QELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 SSGLDLPSELVQELIPEQQDPLKKIKSDMKG-SIGNITVDMVLGGMPGMTGLLWKPHYLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                        EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TPACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CARYOPHYLLIDAE; CARYOPHYLLALES; CHENOPODIACEAE; BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 IPDHV-YKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 IAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLEL-MRLYVTIHSDH
                                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                                                                                                                                                                                             LA COGNATA II., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER PLANT CELL PHYSIOL. 0:0-0(0).
-i- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE (SI)-SYNTHASE (EC 4.1.3.7) (CONDENSING ENZYME)
(CITRATE OODENSING ENZYME) (CITRAGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2637; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 AA; 48881 MW; 003588CE CRC32;
    437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00285; citrate_synt; 1.
MENDEL; 15201; BETvu;2977;mn15201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D4259 PRELIMINARY;
024259;
01-JAN-1998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 LERPKSVTMEWLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 LERPKSVTMEWLENGCKK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 81.3%;
nes 356; Conservative
                                                                                                                                                                                       BETA VULGARIS (SUGAR BEET)
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X84228; E137433; -
    PRELIMINARY;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              OXALOACETATE
                                                                                                                                                (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                     096544;
096544
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; FRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
             POPULUS DELTOIDES X POPULUS BALSAMIFERA SUBSP, TRICHOCARPA.
EUKARYOTA, VIRIDIPLANTAE, STREPTOPHYTA, EMBRYOPHYTA, TRACHEOPHYTA;
EUPHYLLOPHYTES, SPERMATOPHYTA, MAGNOLIOPHYTA, EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                 60 KGIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPMNDSLVIGGNFSHMLGFD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 SPEMQEL-MRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 SSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 EVLLWIKSVVEECGENITTEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFALK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 HLPDDPLFQLVSKLYEVVPPVLTQLGKVKNPWPNVDAHSGVLLNYYGLTEARYYTVLFGV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 VPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYE 194
                                                                                                                                                                                                                                                                                                                                                          1 MPTKEQVGALSKELRDRALVHDYV-FKAIDALPVIAHPMIQFAIGVMALQVQSEFQKAYE 59
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and sequence analysis of human citrate synthase cDNA.";
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                      LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER PLANT CELL PHYSIOL. 0:0-0(0).
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                        Length 339;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                  Match 59.7%; Score 2068; DB 10;
Local Similarity 81.7%; Pred. No. 0.00e+00;
les 276; Conservative 35; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 SRSIGICSQLIWDRALGLPLERPKSVTMELLENHCKKA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 SRALGICSQLIWDRALGLPLERPKSVIMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C0532604 CRC32;
                                                                                                                                                                                                                                                  339 AA; 37834 MW; B2DA24A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO OTHER CITPATE SYNTHASES EMBL; AF047042, G1288815, ...
PROSITE: PSO0480: CITFATE_SYNTHASE; 1.
LYASE: PSO0480: CITFATE_SYNTHASE; 1.
SEQUENCE: 466 AA; 51706 MW: C0532604 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TREMBLREL. 08, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                            EMBL; X84227; E275838; -. PFAM: PF00285; citrate_synt; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITRATE SYNTHASE (EC 4.1.3.7).
                                                                     VIOLALES: SALICACEAE; POPULUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOLDENTHAL M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXALOACETATE.
                                                                                                                                                                             OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-HEART;
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                        Query Match
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54.7%; Score 1897; DB 4; Length 466;

Query Match

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                                                                                                                                                                                                                                                                                                                                   88 LLIYGELPSSEQYNNFTKKVAVHSLVNERLHYL-FQTFCSSSHPMAIMLAAVGSL---SA 143
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                                                                                                                                                                                                                                                                                    86 DPDEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 IISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMN 212
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                                                                                                                           27 SASSINLK-DILADLIPKEQARIKTFRQQHGKTVVGQITVDMMYGGMRGMKGLVYETSVL 85
                                                                                                                                                                                                   34 TSSGLDLRSELVQELIPEQQDRLKKIKSDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYL 92
                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 ALPSHVV-TMLDNFPTNLHPMSQLSAAVTALNSESNFAQAYARGISRTKYWELIYEDSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 LIAKLPCVAAKIYRNLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTEL-MRLYLTIHS
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                                          84; Mismatches 86; Indels
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RODCIT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; US9712; G1390003; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
Best Local Similarity 59.3%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 AA; 46189 MW; 9CCB3291 CRC32;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANN
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Q53115;
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                                                          312 LRAAVLKETCKEVLKELGQLDGNPLLQIAIEL-EAIALKDEYFIERKLYPNVDFYSGIIY 370
                                                                                      358 LRKTVPRYTCQREF-AMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
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                            300 ALNGLAGPLHGLANQEVLLWIKSV--VEECGENISKEQLKDYVWKTLNSGKVVPGFGHGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.6%; Score 264; DB 2; Length 411; Best Local Similarity 28.0%; Fred. No. 2.91e-27; Matches 90; Conservative 91; Mismatches 112; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HA-91;
RADKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: CITPATE + COA = ACETYL-COA + H(2)Q +
                                                                                                                                                                                                                                                                                                                               BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TPEMBLPEL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
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                                                                                                                                                                                                            411 AA
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-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                             RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: U59731; G1390011; --
PROSITE: PSOMAGO; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt, 1.
LYASE: IRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                            PRT;
                                                                                                                                          417 NYYGLTEARYYTVLFGVSRALG 438
                                                                                                                    371 KAMGIP-SQMFTVLFAIARIVG 391
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189 FQKAYEKGIHKSKYWEDIYE-DSMNLIAQVPLVAAYVYRRMYKNGDI-IPKDESLDYGAN 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 F---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNSLDFTEN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 FLHMMFATPCTKYKVNPIIKNALNKIFILHADHEQ-NASTSTVRIASSSGANPFACISTG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 IASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 LNGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYVWKTLNSGKVVPGFGHGVL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 RAAVLKETCKEVLKELGQLDNNPLLQIAIEL-EAIALKDEYFIERKLYPNVDFYSGIIYK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 RKTVPRYTCQREF-AMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLLN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .Match 7.6%; Score 263; DB 2; Length 411;
Local Similarity 28.0%; Pred. No. 4.49e-27;
les 90; Conservative 91; Mismatches 112; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                STRAIN-M S\6;
ROUX V., RYDKINA E., EREMEEVA M., RAOULT D.;
SUBMITTED (COCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNHHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                            BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; PICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                            01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AA; 45266 MW; A54EAICF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 AA
                            411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: TO OTHER CITRATE SYNTHASES. EMBL; U74756; G1658283: -- PROSITE; PSO0480; CITRATE_SYNTHASE; 1. PFRAM; PFRO285; citrate_synt; 1. LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                            CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: TRICARBOXYLIC ACID CYCLE
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 YYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AMGIP-SQMFTVLFAIARTVG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-PUERTO RICO:
                                                                                                                                                                                                                     RICKETISIA MONTANA.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RICKETISIA SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
LT 10
P77936
P77936;
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054382
054382;
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Score 261; DB 2; Length 356;
Pred. No. 1.07e-26;
92; Mismatches 112; Indels 29; Gaps 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 9804343.
KEDNK H.-P. CLAYTON P. A. TOMR J.-F. WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D. L. KEPLANAGE A.P., GRANAD E.E., KYPRIDES N.C.,
FLEISCHAANN P.D. OTMATENRUSH J. LEE N. H., SUTTON G.G.LL S.
KIRKNESS E.F., DOUGHEPTY B.A. MCKENNEY K., ADAMS M.D., LOPTUS B.,
KIRKNESS E.F., DOUGHEPTY B.A., MCRENNEY K., ADAMS M.D., LOPTUS B.,
COTTON M.D., SPRIGGS T., MEIDMAN J.F., MCDONALD.L., UTIERBACK T.,
COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
SADOW P.M., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MAGNN T. M., OLSEN G.T., FPRASEP C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 LLLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTOFATGVMALQVQSE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 F---YP-DLLNF-FKEADYELTAIRMIAKIPTIAAMSYK--YSIGQPFVYPDNSLDFTEN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 FQKAYEKGIHKSKYWEPTYE-DSMNLIAQVPLVAAYVYRRMYKNGDTIP-KDESLDYGAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 FLHMM-FATPCEKYKVNPVVKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACVST 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 GIASLWGPAHGGANEAVINMLKDIGSVENIPKYIAKAKDKNDNFRLMGFGHRV--YKNYD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 LRKTVPRYTCQREF-AMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPWPNVDAHSGVLL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 ALNGLAGPLHGLANQEVLLWIKSV--VEECGENISKEQLKDYVWKTLNSGKVVPGFGHGV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 PRAAVLKETCKEVLKELGQLDNNPLLQIAIEL-EAIALKDEYFIERKLYPNVDFYSGIIY 327
                                                                                                                                                                                                                                                                                                                                                                                                                                            44 LLIYGELPNSKQYNDFTKKVAHHALVNERLHYL-FQTFCSSSHPMAIMLAAVGSL---SA 99
               DAVIS M.J., YING Z., BRUNNER B.R., PANTOJA A., FERWERDA F.H.; "Rickettsial relative associated with papaya bunchy top disease."; CURP. MICPOBIOL 36:80-84(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 FAHMLGFSSS-EMHEL--LMR--LY-VII-HSDHEGGNVSAHTGHLVASALSDPYLSFAA
                                                                           1- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                                         -! - CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The complete genome sequence of the hyperthermophilic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                         356 AA; 40030 MW; 15BF55D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AA
                                                                                                                                                                                      TO OTHER CITRATE SYNTHASES.
                                                                                                                                                                                                     EMBL; U76908; G2894/9/;
PROSITE: PSON480; CITRATE_SYNTHASE; 1.
LYASE: TRICARBOXYLIC ACID CYCLE.
                                                                                                                       ** PATHWAY TRICARROXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 NYYGLTEARYYTVLFGVSRALG 438
                                                                                                                                                                                                                                                                                                                                                        Match 7.5%;
Local Similarity 27.6%;
es 89; Conservative
                                                                                                                                                                                                   U76908; G2894797; -
                                                                                                                                                                  OXIDATIVE METABOLISM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARCHAEOGLOBUS FULGIDUS.
MEDLINE; 98087556.
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                                                                                                   OXALOACETATE
                                                                                                                                                                                      -1- SIMILAPITY.
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                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
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028929
028929;
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Pred. No. 1.07c-26; 77; Mismatches 114; Indels 22; Caps 16;
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                                                                                                                                                                                                                                                                                                        173 MIQFAIGVMALQVQSEFOKAYEKGIHKSKYWEPTYEDSMNLIAQVFLVAAYVYRRMYKNG 232
                                                                                                                                                                                                                                                                                                                                                    142 RNIIPPALEFSHAANFLYMLHGEEPTKTAERALDMDLILHAEHEL-NASTFAARIAASTL 200
                                                                                                                                                                                                                                                                                                                                                                                               233 -DIIPKDESLDYGANFAHML-GFSSSEMHELLMRLYVTIHSDHEGGNVSAHTGHLVASAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                           201 ADIYACVVAATGTLMGPLHGGAAQEVM---R-MLREVASP-RRAE--EYVKRKIEAGERI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 SDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEEGGENISKEQLKDYVWKTLNSGKVV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 LLIYGELPSGEQYNNFTKQVAHHSLVNERLHYL-FQTFCSSSHPMAIMLAAVGSL---SA 143
                                                                                                                                                                                                                                                               85 LPPYTHPMVVLRTATSYLGSLDKKIA-VRTREETFNKAKDLIAKFPTIVAY-YHRI-RTG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 MGFGHRVYRGVMDPRAELLR-YLAKRLAAEG----STKWFEISEAIAKAAYKYKLLPNV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 PGFGHGVLRKTV-PRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLKPW-PNV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 LLLIGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 7.5%; Score 260; DB 2; Length 411; Local Similarity 27.7%; Pred. No. 1.64e·26; hes 89; Conservative 92; Mismatches 112; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NTT-118;
RACCLI D., RYDKINA E., ROCX V., EREMEEVA M., BALAYEVA N.,
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OXIDATIVE METABOLISM.
-1- CATALYIIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 DFYSASVYANLGIPDDLFVNI-FAMGRISGWTAHII-EQYENNRLIRPRA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 DAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKS 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                    / Match 7.5%; Score 261; DB 1; Length 372; Local Similarity 26.6%; Pred. No. 1.07c-26; les 77; Conservative 77; Mismatches 114; Indels 3:
sulphate-reducing archaeon Archaeoglobus fulgidus.";
NATURE 390:364-370(1997).
BMBL: A90:01011; G2649234; -.
IIGR: AF1340; -.
IFGR: AF1340; -.
PFAM: PF0028B; citrate_synt; 1.
SEQUENCE 372 AA: 42270 MW: DB9662BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 AA; 46095 MW; 274AAD7C CRC32;
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-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; U59726; 61390019; -.
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
PFAM; PFRO0285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THAI TICK TYPHUS RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SEQUENCE
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Q60047
Q60047;
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Gaps 20
                                                                                         247 FAHML-GFSSSE--MHELLMR-LY-VII-HSDHEGGNVSAHIGHLVASALSDPYLSFAAA 300
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                                                                                                                                                                                   IASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDP 312
                                                                                                                                                                                                                                             301 LNGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYVWKTLNSGKVVPGFGHGVL 358
                                                                                                                                                                                                                                                                                                                                             129 LLLIGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSE 188
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                                                            196 FLHMMFATPCTKYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTG 254
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Local Similarity 28.3%; Fred. No. 2.53e.26;
les 91; Conservative 89; Mismatches 113; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ISTT CDC1;
RADKINA E., FOUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
--- CITRATE SYNHARSE IS FOUND IN NEARLY ALL CELLS CAFABLE OF
OXIDATIVE METABOLISM.
---- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7.7) (FRAGMENT).
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88 LLIYGELPSGEQYNNFTKQVAHHSLVNERLHYL-FQTFCSSSHPMAIMLAAVGSL---SA 143
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                                                                                                                                                                                                                                                                                                                                             STRAIN-STRAIN S;
RAOULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (UNN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYMTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                   BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 7.4%; Score 258; DB 2; Length 411; Local Similarity 28.0%; Fred. No. 3.89e-26,
                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90; Mismatches 113;
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                                                                                                                411 AA
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-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; U59735; G1390015; -.
PROSIE: FSO0480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                          CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
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                                                                                                                                                     CREATED)
                                                                                                                PRT;
                                  418 YYGLTEARYYTVLFGVSRALG 438
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372 AMGIP-SQMFTVLFVIARIVG 391
                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01,
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                                                                                                                PRELIMINARY;
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Q59779;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri Oct 22 16:55:04 1999; MasPar time 6.83 Seconds 749.237 Million cell updates/sec MPsrch\_pp

Run on:

Tabular output not generated.

>US-08-702-718-4 (1-437) from USO8702718.pep 3243 1 SSNLDLRSELQELIPEQQER......LERPKSVTMEWLEKFCKRRA 437 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

119857 seqs, 11713122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Mean 33.342; Variance 155.188; scale 0.215 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	2.02e+01	3.74e+01	3.74e+01	3.74e+01	3.74e+01	3.74e + 01	4.36e+01	4.36e+01	4.36e+01	5.90e+01	4.36e+01	4.36e+01	4.36e+01	1.07e+02	6.85e + 01	1.07e+02	1.07e±02	1.07e+02	9.24e+01	1.07e+02	1.07e+02	1.07e+02	1.07e+02
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Description	Sequence    Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence							
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SEQUENCE CHARACTERISTICS:

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224 LELMRL-YVTIHS 235

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                                                             283 WIKSVVDECGENISTEQLKDYVW-KTL-NSGKVVPGFGLGVLRKTDPRYTCQREFALKHL 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 NKSWQPSFV-CGKLFETIPLTTV-DYKHLLKQ-KVLPGQDHPESARSLLQHKSSFVSPPP 212
                                                            Ouery Match 3.0%; Score 97; DB 2; Length 624;
Best Local Similarity 25.3%; Pred. No. 2.02e+01;
Matches 21; Conservative 21; Mismatches 34; Indels 7; Gaps
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                                                                                                                                                                                                                                                                                                            APPLICANT: Cochran Ph.D., Mark D
TITLE OF INVENTION: Recombinant Equine Herpesvirus
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MM-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07424
FILING DATE: 19930806
CLASSIFICATION:
                                                                                                                                                                                                          324 AA.
                               .OGY: linear
624 AA; 69538 MW; 1929028 CN;
                                                                                                                                                                                                          PRT;
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MOLECULE TYPE: protein
HFNCE 324 AA; 36456 MW; 559982 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FEATABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      Sequence 4, Application PC/TUS9307424
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 4, Application PC/TUS9307424
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: John P. White STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: White, John P
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELERAX: (212)564-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                            146 WEAHPFFNFIKRQYQINAQALQE 168
                                                                                                                                                            341 -PDDPFFQLVSKLYEVVPILLE 362
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amino acid
624 amino acids
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
          TYPE: amino acid STRANDEDNESS:
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PCT-US93-07424-4
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LENGTH:
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156 NKSWQPSFV-CGKLFETIPLTTV-DYKHLLKQ-KVLPGQDHPESARSLLQHKSSFVSPPP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 2.9%; Score 93; DB 1; Length 324; Best Local Similarity 24.7%; Pred. No. 3.74e+01; Matches 18; Conservative 24; Mismatches 25; Indels
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
TITLE OF INVENTION: Recombinant Equine Herpesvirus
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,094
FILING DATE: February 17, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 AA.
                  324 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 324 AA; 36456 MW; 559982 CN;
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application PC/TUS9502087
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application PC/TUS9502087
                                                                                                                                                                      Sequence 4, Application US/08198094 Patent No. 5741696
                                                                                                                                                                                                                                                                                                             ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New YORK
COUNTRY: USA
                                                                                                                                     Sequence 4, Application US/08198094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)664-0525
TELEX: 422523
INFOFMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 -NFKRLIYAVVDP 224
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PCT-US95-02087-4
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                US-08-198-094-4
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                                                          XXXXX
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
IITLE OF INVENTION: Recombinant Equine Herpesviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 2.9%; Score 93; DB 3; Length 324; Best Local Similarity 24.7%; Pred. No. 3.74e+01; Matches 18; Conservative 24; Mismatches 25; Indels
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Patent No. 5731188
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
TILLE OF INFORMEN: Recombinant Equine Herpesvirus
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AA.
                 NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE 324 AA; 36456 MW; 559982 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/198,094
FILING DATE: FEBRUARY 17, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECHONIC (212)278-0400
TELEFRAX: (212)391-0525
TELERAX: 42253
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08323531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 324 amino acids amino acid
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                                                                                                            New York
: USA
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New York
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US-08-323-531-4
                                                                                                                              COUNTRY:
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STATE:
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156 NKSWQPSFV-CGKLFETIPLTTV-DYKHLLKQ-KVLPGQDHPESARSLLQHKSSFVSPPP 212
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APPLICANT: Calhoon, Roger D
APPLICANT: Calhoon, Roger D
APPLICANT: Calfand, David H
APPLICANT: Fear, Anna L
APPLICANT: Meade, James H
APPLICANT: Tal, Rony
APPLICANT: Tal, Rony
APPLICANT: Benziman, Moshe
TITLE OF INVENTION: METHODS AND NUCLEIC ACID SEQUENCES FOR THE
TITLE OF INVENTION: EXPRESSION OF CELLULOSE SYNTHASE OPERON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 1; Length 324;
Pred. No. 3.74e+01;
24; Mismatches 25; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
COUNTRY: Usa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3031 AA.
                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/926,784
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
JENCE 324 AA; 36456 MW; 559982 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI,
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEFAX: 422523
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/07689008
Patent No. 5268274
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/07689008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.9%;
Best Local Similarity 24.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 LELMRL-YVTIHS 235
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RESULT
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Applicant Stephen R.
APPLICANT: Stallings, William C.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                   464 FWSEVYETTMALFLVRVTIITLMFPSKGKFNVTEKGGVLEEEEFDLGATYPNII-FAGIM 522
                                                                                                                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                     Score 93; DB 1; Length 3031; Pred. No. 3.74e+01; 30; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 61198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             430 AA.
                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 3031 AA; 328497 MW; 44365167 CN;
APPLICATION NUMBER: US/07/689,008 FILING DATE: 19910422 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 337,194 FILING DATE: 12-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/833,485
FILING DATE: 07-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                              US 496,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44, Application US/08833485
Patent No. 5804425
GENERAL INFORMATION:
                                                                                                             NAME: Murphy, Lisabeth Feix
REGISTRATION NUMBER: 31547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 393-2000
TELEFAX: (415) 393-2286
TELEX: 340817 MACPAG SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3031 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08833485
                                                                                         FILING DATE: 23-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                              523 TLGLLIGLFELTFHFNQLAG 542
                                                                                                                                                                                                                                                                                                                                                                                223 MLELMR-LY-VTIHSDHEGG 240
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      Query Match 2.9%;
Best Local Similarity 20.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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STREET: 700 ...
CITY: St. Louis
                                                                                                                                                                                                                 TYPE: AMINO ACID
                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-833-485-44
                                                                                                                                                                                                                           TOPOLOGY
                                                                                                                                                                                                                                                  SEQUENCE
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Sequence 44, Application US/08306063
Patent No. 563445
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Rishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 YKPLLGEDCRRIMDIFRHLGVEIKEDDEKLVVIS-PGYQVNIPHQVLYIGNSGTITRLLA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92; DB 2; Length 430;
Pred. No. 4.36e+01;
15; Mismatches 31; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/306,063
FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                  38-21(15117)A
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 430 AA; 46852 MW; 962324 CN;
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEFAX: (314)737-6099
TELEFAX: (314)737-604
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/08306063
                                                                                                                                                                                                                                                                                                                                                        : 430 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.8%;
Best Local Similarity 31.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 700 Chestern St. Louis STATE: Missouri COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 GLLSGLGNESVL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 GPLHGLANQEVL 281
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                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
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                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: HOETNEY Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELEPHONE: (314)537-604
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                          Query Match 2.8%;
Best Local Similarity 31.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 800
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                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                       270 GPLHGLANQEVL 281
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US-08-737-524B-27
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                  : :|| | : ::: | | | | | | | :: | | 3.3 FAHMLGFDSPQMLELMR-LYVTIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGL-A 269
                                                                                                                                                                                                                                                                                                                   43 YKPLLGEDCRRTMDIFRHLGVEIKEDDEKLVVTS-PGYQVNTPHQVLYTGNSGTTTRLLA 101
                                                                                                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                              15; Mismatches 31; Indels
                                                                                                                                                                                                                                                                        Score 92; DB 1; Length 430;
Pred. No. 4.36e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   430 AA.
                                                                                                                                    38-21(10660)A
                     APPLICATION NUMBER: US 07/749,611 FILING DATE: 28-AUG-1991 CLASSIFICATION: 435
                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 PPT;
                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 430 AA; 46852 MW; 962324 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 44, Application US/08476008 Patent No. 5627061 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 44, Application US/08476008
                                                                                                                                                        TELEPHONE: (314)537-6099
TELEEA:: (314)537-6047
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
                                                                                                                           30,914
                                                                                                                                   REFERENCE/DOCKET NUMBER: 38 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                        Query Match 2.8%;
Best Local Similarity 31.9%;
Matches 23; Conservative
           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                               102 GLLSGLGNESVL 113
                                                                                                                                                                                                                                                                                                                                                                                      270 GPLHGLANQEVL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63198
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                                                                                                                                                                                                                                                  SEQUENCE
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 88888888888888888888888888888888
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212 FAHMLGFDSPQMLELMR-LYVITHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGL-A 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/08737524B
Patent No. 5912414
GENERAL INFORMATION:
APPLICANT: CARL SAVERIO FALCO
APPLICANT: DOMINICK ANTHONY GUIDA, JR.
APPLICANT: MARY ELIZABETH HARNETT LOCKE
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC
TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
TITLE OF INVENTION: OF PLANTS
TITLE OF INVENTION: OF PLANTS
WUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92; DB 1; Length 430;
Pred. No. 4.36e+01;
15; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USE: E. I. DU PONT DE NEMOURS AND COMPANY P. 1007 MARKET STREET WILLMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READMALE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,524B
                                                                                                                                                                                    38-21(10660)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 430 AA; 46852 MW; 962324 CN;
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5; Caps
                                                                                                                                                                                                                                                                         415 IAKSQMTGF-GGVVSFEVAGDFDATRKFIDSV-KIPYHAPSFGGCESIIDQ-PAIMSY 469
                                                                                                                                                                                                                                                                                                  133 ITAHPMTQFCTGVMALQTRSEFQ--KAYEKGIHKSKFWEPTYEDCLSLIAQVPVVAAY 188
                                                                                                                                                                                                                     Score 90; DB 2; Length 509; Pred. No. 5.90e+01; 18; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDDRONATE 2-SULFATASE
CORPRESPONDENCE: 15
CORPRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                      510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY.

ZIP: 11530
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk

~WETTER: IBM PC compatible

~WETTER: """TEM: PC-DOS/MS-DOS
        NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REPERENCE/POCKET NUMBER: RB-1059-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 509 AA: 54816 MW; 1292600 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/484,494
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08484494
Patent No. 5798239
GENERAL INFORMATION.
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, FRANK S
REGISTRATION NUMBER: 31,346
PREPERICE/POCKET NUMBER: 84167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08484494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
                                                                                   TELEX: 835420
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                           LENGTH: 509 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9
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Local Similarity 25.9%;
hes 15; Conservative
                                                                                                                                                        single
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CITY: Garden City
                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                     US-08-484-494-11
                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                 27 EFGSFQLGNINVD-M-VLGGMRGMTGLLWETSLLDPEEGIRFRGFSIPECQKLLPAAS 82
                                                                                                                                                                          3;
                                                                                                                                              . Match 2.8%; Score 92; DB 2; Length 510; Local Similarity 27.6%; Pred. No. 4.36e+01; les 16; Conservative 16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Occhiodoro, Teresa
APPLICANT: Glements, Peter P
APPLICANT: Hopwood, John J
TITLE OF INVENTION: IDURONATE 2-SULFAINE OF
TITLE OF INVENTION: IDURONATE 2-SULFAINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                510 AA
                                                                                                       MOLECULE TYPE: protein
JENCE 510 AA; 57860 MW; 1366158 CN;
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLING LDAIL:
CLASSIFICATION: 435
PRICR APPLICATION DATA
APPLICATION NUMBER: 991.973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 41167
TELECOMMUNICATION INFORMATION:
TELECAX: 516-742-4343
TELEXX: 516-742-4343
INFORMATION FOR SED ID NO: 11:
SEQUENCE CHAPACTERISTICS:
LENGTH: 510 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                       Seguence 11, Application US/08345212
                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08345212
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID 00: 11:
SEQUENCE CHARACTERISTICS:
                                                   LENGIH: 510 amino acids
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 15
CORPESPONDENCE ADDRESS:
                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 400 CLTY: Garden City CTTY: Garden City
                                                                                            TOPOLOGY: linear
                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 593<u>2</u>211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11530
                                                                                                                                                                                                                                                                                US-08-345-212-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                     SEQUENCE
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                          XXXXXX
                                                                                                                                                                       Matches
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 8888888888888
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3; Gaps
                                                                                                                 338 DIAGYDLNKTQMDGMSLLPILRGASNLTWRSDVLVEYQGEG-RNVTDPTCPSLSPGVS 394
                                                                                                                               Score 92; DB 2; Length 510;
Pred. No. 4.36e+01;
16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFIGURATION OF A COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTHER: IBM PC compatible
COMPOTHER: DATE OF COMPACTION OF SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: 07-010-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Morris, Charles P
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald'S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: HOPWOOd', John J
IITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF EXQUENCES: 15
CORRESSEDNDENCE ADDRESS:
ADDRESSEDE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                                                                              510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 510 AA; 57860 MW; 1366158 CN;
           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 510 AA; 57860 MW; 1366158 CN;
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08484493
Patent No. 5728381
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          Sequence 11, Application US/08484493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 841
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 516-742-4343
TELEFRAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 510 amino acids
                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
single
                                                              Query Match 2.8%;
Best Local Similarity 27.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 400 Garder
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
STRANDEDNESS:
                                                                                                                                                                                              US-08-484-493-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                       338 DIAGYDLNKTQMDGMSLLPILRGASNLTWRSDVLVEYQGEG-RNVTDPTCPSLSPGVS 394
                                                        27 EFGSFQLGNINVD-M-VLGGMRGATGLLWETSLLDPEEGIRFRGFSIPECQKLLPAAS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 LKWMGWKNTNTGESTHVEEFKGRVTMSLDTSTNTAYMELSSLRSEDTAVYYCAREY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 LIMIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPR-YTCQREF 335
                                                                                                                                                                                                                                                                                                       APPLICANT: SHIOSKII, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
 Pred. No. 4.36e+01;
16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86; DB 2; Length 119;
Pred. No. 1.07e+02;
13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
                                                                                                                      119 AA
                                                                                                                                                                                                                                                                                                                                                                                                       E: Browdy and Neimark
419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE 119 AA; 13166 MW; 84737 CN;
                                                                                                                                                                                                                          Sequence 10, Application US/08491845
Patent No. 5773247
GENERAL INFORMATION:
APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: EDA, Yasuyuki
                                                                                                                                                                                                     Sequence 10, Application US/08491845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: MATELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 119 amino acids
amino acid
                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7%;
ilarity 28.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
Best Local Similarity 27.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
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nes 16; Conserv
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US-08-491-845-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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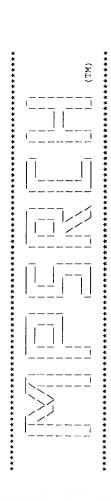
DB 1; Length 510;

Score 92;

2.8%;

Query Match

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259 LSFAAALNGL-AGPL-HGLANQEVLLWIK-SVVDE-CGENISTEQLKDYVWKTLNSGKVV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 LSLSLLLPLLKSGSLGAALLRNGVLMSLTFPILPIIYQQKIMMHIGKDYSWLGLVTGEVI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.7%; Score 89; DB 2; Length 230;
Best Local Similarity 30.3%; Pred. No. 6.85e+01;
Matches 20; Conservative 16; Mismatches 26; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPPRATING SYSTEM PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION 3-MAY-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATE: US/08/637,759B
FILING DATE: 11-DEC-1995
CLASSIFICATION 1435
APPLICATION WINBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: BADSt, Patrea L.
REGISTRATION NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPAX: (404) 873-8794
TELEPAX: (404) 873-8795
INFORMATION FOR SEQ 1D NO: 457:
SEQUENCE CHARACTERISTICS:
 230 AA.
                                                                                                           Sequence 457, Application US/08637759B
Patent No. 5876931
GENERAL IMPORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
 PRT;
                                                                                                                                                                                                                   ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
ENCE 230 AA; 25640 MW; 291720 CN;
                                                                                    Sequence 457, Application US/08637759B
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 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM - MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 30309-3450
US-08-637-759B-457
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 16:49:12 1999; MasPar time 19.68 Seconds 889.641 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-4 (1-437) from USO8702718.pep 3243 1 SSNLDLRSELQELIPEQQER......LERPKSVIMEWLEKFCKRRA 437 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

122810 segs, 40068593 residues

Searched:

1:pirl 2:pir2 3:pir3 4:pir4 pir60 Database:

Mean 49.482; Variance 97.811; scale 0.506 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	1. No.	.00e+00	00e+00	00e+00	.00e+00	.00e+00	0.00e+00	.coe+00	.00e+00	.20e-269	.20e-229	.51e-37	.28e-37	.45e-34	.24e-34	.44e-33	.04e - 31	.11e-30	15e-27	.14e-26	.12e-26	.94e-23	.25e-22	09e-22
	Pred.	0.	0.0	0.	0	0.0	0.	0.0	0.0	2	7	ω.	2	1.4	10	4.4	7	٦	2.	1.1	9.	1.5	~	5.
	Description	probable citrate (si)	ethanolamine ammonia-	citrate (si)-synthase	14-nm filament protei	citrate (si)-synthase	citrate synthase - Ba	citrate (si)-synthase	citrate (si)-synthase	citrate (si)-synthase	citrate synthase III	citrate synthase gltA	probable gltA2 protei	citrate synthase (cit	citrate (si)-synthase	citrate (si)-synthase	citrate (si)-synthase	citrate synthase - cu	citrate (si)-synthase					
SUMMARIES	1D	T02390	544316	YKMUM	YKPG	S42370	YKBY	S41563	YKBYC	JC5625	S52814	A43936	140717	YKQPC	YKPSCA	E69658	S74344	E70782	C69417	JQ1392	I39506	YKEC	S53007	E64760
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-	rength	474	471	472	464	468	479	469	460	462	486	373	437	436	428	372	397	431	372	430	424	427	516	389
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	score	2834	2637	2249	2096	1890	1815	1761	1701	1451	1261	323	324	309	306	301	292	288	270	266	261	248	C 7 C 1	240
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231 7.1 372 224 6.9 426 215 6.6 446 216 6.8 426 192 5.9 429 192 5.9 362 168 5.2 385 158 4.9 373 129 4.0 373 129 4.0 373 120 3.1 344 101 3.1 1382 106 3.3 901 101 3.1 1382 102 3.1 1382 102 3.1 1161 102 3.1 1382 103 3.1 1382 104000  Example of the land of the l	20 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		ttype c crate (	tein **Seque 39 .D.; Li: R.C.; S;	thali thali inary; ##labe 53/3;	lyas #mole ; Sc ; Pr	CKLK   :   KIK	COKVLPTAQSGABPLPEG    :  :  :    COKLLPAASAGABPLPEG TAHPMTQFASGVMALQVQ    :    :   :
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H O D O D O D O D O D O D O D O D O D O	, 4000000000000000000000000000000000000	4 4 4 4 4	RESULT ENTRY TITLE ALTERNA	ALTERNA ORGANISI DATE ACCESSI REFEREN	sub accaccaccaccaccaccaccaccaccaccaccaccacc	#not EYWORL UMMARY Query Best Match	Db Qy	0 O Y D D D D D D D D D D D D D D D D D D

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                                                                              276 NVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQL 335
                                                                                                                                                                                                    301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                  361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ethanolamine amonia-lyase (EC 4.3.1.7) - potato
#formal_name Solanum tuberosum #common_name potato
08-Sep-1994 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
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                                      181 OVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEGG
                                                                                                    336 KEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQREFALKHLPDDPLFQLVSKLYEVVPPVL
                                                                                                                                                                                                                                            396 TELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLALER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:X75082; NID:9483509; PID:9483510
FICATION #superfamily citrate (si)-synthase
ammonia-lyase; carbon-nitrogen lyase
#length 471 #molecular-weight 52612 #checks:
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Pred. No. 0.00e+00;
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Best Local Similarity 81.3%;
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#authors Unger, E.A.; Hand, J.M.; Cashmore, A P : Vasconcelos, A C.
#journal plant Mol. Biol. (1989) 13:411-418
#title isolation of a cDNA encoding mitochondrial citrate synthase
from Arabidopsis thaliana.
#cross-references MUID:91370823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 SCLIELES-EEPWPNVDAHSGVLLNHYGLIEARYYTVLFGVSRSLGICSQLIWDRELLLA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 EEVFALGDCFLPECOKALLPTAQSGGLNHYPRSFVASLNWKGTL-AKSKLKH-CPKTWNP 153
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                                                                                   #formal_name Arabidopsis thaliana #common_name mouse-ear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #region acetyl-CoA binding #status predicted\
#active_site His, His, Asp #status predicted
#length 472 #molecular-weight 52941 #checksum 9626
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&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *superfamily citrate (si)-synthase
carbon-carbon lyase; homodimer; mitochondrion;
oxo-acid-lyase; tricarboxylic acid cycle
                                      citrate (si)-synthase (EC 4.1.3.7) precursor, Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 69.3%; Score 2249; Local Similarity 71.7%; Pred. No. 0.
                      #type complete
                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
#*rocidues 1-472 ##label UNG
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309,355,407
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                                                                                                                                                                                                        annotation; X-ray crystallography, 2.7 and 1.7 angstroms Citrate (si)-synthase is found in nearly all cells capable of oxidative metabolism. It catalyzes the condensation of oxaloacetate and acetyl-coA to form citrate in the tricarboxylic acid cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrion of eukaryote cells. This molecule is a dimer of identical chains. Each dimer binds two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecules of acetyl-CoA and two molecules of oxaloacetate at two
                                                                                         citrate (si)-synthase (EC 4.1.3.7) precursor - pig
#formal_name Sus scrofa domestica #common_name domestic pig
15-oct-1982 #sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #active_site His, His, Asp #status predicted\
#modified_site N6,N6,N6-trimethyllysine (Lys) #status
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*product citrate (si)-synthase *status experimental *label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Wade, R.D.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.; Titani, K. Proc. Natl. Acad. Sci. U.S.A. (1981) 78:5381-5385 Primary structure of porcine heart citrate synthase. A61347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carbon-carbon lyase; homodimer; methylated amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                        Bloxham, D.P.; Parmelee, D.C.; Kumar, S.; Walsh, K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete amino acid sequence of porcine heart citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7 angstroms resolution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2096; DB 1; Length 464; Pred. No. 0.00e+00;
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J. Mol. Biol. (1982) 158:111-152
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Biochemistry (1982) 21:2028-2036
                                                                         #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-464 ##label BLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type protein
##residues 28-464 ##label BL2
                                                                                                                                                                       A29966; A01109; A61347
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418 LERPKSVTMEWLEKFCKR 435
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28 ASSTNLKDILADLIPKEQARIKTFRQQHGNTVVGQITVDMMYGGMRGMKGLVYETSVLDP 87

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S42370 #type complete
citrate (s1)-synthase (EC 4.1.3.7) precursor - Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 VAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAELMRLYLVIHSDHEGGNVS 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 GNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PDHVYKTIDALPITAHPMIQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                 268 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 LRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 LLEOGKAKNPWPNVDAHSGVLLQYYGMTEMNYTTVLFGVSRALGVLAQLIWSRALGFPLE 447
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                                                                                          88 DEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAAL 147
                                                                                                                                                                                                                148 PSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIA 207
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#formal_name Caenorhabditis elegans
07-0ct-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                208 KLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEG
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EMBO J. (1984) 3:1773-1781
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             citrate (si)-Synthase (EC 4.1.3.7) precursor, mitochondrial yeast (Saccharomyces cerevisiae) protein NVO19: protein VNO01c #formal name Saccharomyces cerevisiae 25-Feb-1985 *sequence_revision 10-Feb-1995 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545118
Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
Verhasselt to the EMBL Data Library, January 1994
Twelve open reading frames revealed on the 23.6 kbp segment
flanking the centromere on the Saccharomyces cerevisiae
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**note
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Yeast (1994) 10:1355-1361
Twelve open reading frames revealed in the 23.6 kb segment
flanking the centromere on the Saccharomyces cerevisiae
                                                                                                                                                                                                                               274 AHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFNYTEEQLKEW 333
                                               244 AHTGHLVGSFLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDY 303
                                                                                                    334 VWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSTLYKITPGILLEQ 393
                                                                                                                                                  304 VWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLEL 363
                                                                                                                                                                                                    394 GKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARGMGLPLERPK 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross_references EMBL.X77395; NID:9496717; PID:9496718
NCE S48338
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835390
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##residues
1-57,'O',59-77,'E',78-479 ##label S
##cross-references GB:X00782; NID:93602; PID:93603
##experimental_source strain D273-10B
SNCE
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**residues 1-479 **label LIN
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**residues 1-479 **label VER
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*accession A01110
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#submission

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**cross·references EMBL.Z71616; NID.g1302468, FID.e239778; PID.g1302469; MIPS.YNR001c
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predicted #label TNP\
#product citrate (si)-synthase #status predicted #label
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                                                                                                                                                                                                                                                                                                                                    carbon-carbon lyase; catalyzes condensation of oxaloacetate
and acetyl-CoA to form citrate; oxo-acid-lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSNLDLRSELQELIPPEQGERLKKIKKEFGSFQLGNINVDMVLGGMKGMTGLLWETSLLUP 60
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Neurospora crassa #formal.name Neurospora crassa 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 08-Sep-1997
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#length 479 #molecular-weight 53360 #checksum 4
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                                                                                                                             ##experimental_source strain S288C
                     **#molecule_type DNA 1-479 **label AER 1-479 **
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P.A.; Guarente, L.P.
Mol. Cell. Biol. (1986) 6:4509-4515
Mitochondrial and nonmitochondrial citrate synthases in
Saccharomyces cerevisiae are encoded by distinct homologous
Ferea, T.; Contreras, E.T.; Oung, T.; Bowman, E.J.; Bowman,
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#title Characterization of the cit-1 gene from Neurospora crassa encoding the mitochondrial form of citrate synthase.
#cross-references MUID:94104594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 ELIDRCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLPTI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 KIIDALPITAHPMIQFCTGVMALQIRSEFQKAYEKGIHKSKFWEPIYEDCLSLIAQVPVV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 AARIYONVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELLRLYLTIHTDHEGGNVSA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 HTTHLVGSALSSPFLSVAAGLNGLAGPLHGLANQEVLNWLTEMKKVIGDDLSDEAITKYL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 HTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 WDTLNAGRVVPGYAHAVLRKTDPRYSAQRKFAQEHLPEDPMFQLVSQVYKIAPKVLTEHG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 FRGKTIPECQELLPKAPGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKFIE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosenkrantz, M.; Alam, T.; Kim, K.S.; Clark, B.J.; Srere,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 LKERFAELLPENIEKIKALRKEHGSKVVDKVTLDQVYGGARGIKCLVWEGSVLDAEEGIR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Saccharomyces cerevisiae)
protein YCR005c; protein YCR043
#formal_name_Saccharomyces cerevisiae
30-Sep-1992_#sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                                                                                                                                                                     #length 469 #molecular-weight 52002 #checksum 490
                                                                                                                                                                                                                                                              36/3; 58/2; 123/1; 453/2
*superfamily citrate (si)-synthase
carbon-carbon lyase; mitochondrion; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                    Match 54.3%; Score 1761; DB 2; Length 469; Local Similarity 56.7%; Pred. No. 0.00e+00; es 245; Conservative 81; Mismatches 103; Indels
                                                                                                                                                                                      ##residues 1-469 ##label BOW
##cross-references EMBL:M84187; NID:g168774; PID:g168775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A25393; S26734; S19474; S12944; A39664
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##molecule_type DNA
##molecule_type ]-460 ##label ROS
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#accession A25393
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##molecule_type DNA
##clossreferences EMBL:X59720; NID:g1907116; PID:e264468; PID:g1907148;
##cross-references EMBL:X59720; NID:g1907116; PID:e264468; PID:g1907148;
##cross-references EMBL:X59720; NID:g1907116; PID:e264468; PID:g1907148;
##cross-references EMBL:X59720; NID:g1907116; PID:e264468; PID:g1907148;
                                                                            *authors Biteau, N.; Fremaux, C.; Hebrard, S.; Menara, A.; Aigle, M.; Crouzet, M. *

#journal Yeast (1992) 8:61-70  
#title The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae. #cross-references MUID:92254505  
#accession S26734
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peroxisome; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #region peroxisome location signal (S-[RKH]-L) motif/
#active_site His, His, Asp #status predicted
#length 460 #molecular-weight 51413 #checksum 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 TSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEVLEWLFALKEEVNDDYSKDTIEKYLW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 DILNSGRVIPGYGHAVLRKIDPRYMAQRKFAMDHFPDYELFKLVSSIYEVAPGVLTEHGK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 TKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQLITDRAIGASIERPKSYS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 FRGRIIADIQKDLPKAKGSSQPLPEALFWLLLTGEVPTQAQVENLSADLMSRSELPSHVV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 QLLDNLPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSYTFEDSLDLLGKLPVI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 KTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVV 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 LKERFSEIYPIHAQDVRQFVKEHGKTKISDVLLEQVYGGMRGIPGSVWEGSVLDPEDGIR 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liao, X.; Small, W.C.; Srere, P.A.; Butow, R.A. Mol. Cell. Biol. (1991) 11:38 46
Intramitochondrial functions regulate nonmitochondrial citrate synthase (CIT2) expression in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                    Aigle, M.; Biteau, N.; Crouzet, M. submitted to the Protein Sequence Database, March 1992
##cross-references EMBL:Z11113; NID:q3297; PID:q3299; GB:M14686; NID:q171227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.5%; Score 1701; DB 1; Length 460; Best Local Similarity 53.8%; Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                               translation not shown
                                                                                                                                                                                                                                                                         ##status
##molecule_type DNA
1-460 ##label BIT
1-460 ##1abel BIT
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CLASSIFICATION #su
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#domain transit peptide (mitochondrion) *status
predicted *label TNP\
*product 14-nm filament protein/citrate synthase *status
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**residues

***coss-references GB:D90117: NID:g217406; PID:d1014848; PID:g1688046

***note

mature protein; sequence, including the amino end of the
mature protein, was confirmed by protein sequencing

T This protein is involved in oral morphogenesis preceding binary
fission, and in nuclear events during fertilization, such as
formation of gametic pronuclei and zygote formation of gametic

pronuclei. It also acts as a mitochondrial enzyme, citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Numata, O.; Takemasa, T.; Takagi, I.; Hirono, M.; Hirano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 EGIPFPGFSIPECOKLLP-A-A-SAG-A--EPLPEGLLWLLLTGKVPSKEQVDALSADLP 115
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366 VKNPWPNVDAHSGVLLNHYGLTEAPYYTVLFGVSRSLGICSQLIMDRALGLPLERPKSVT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 SMDLIAKIPRVAAIIYRHKYRDSKLIDSDSKLDWAGNYAHWMGFEQHVVKECIRGYLSIH 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPE 61
                                                                                                                                                                                                                                                                                  14-nm filament protein/citrate synthase (EC 4.1.3.-) -
Tetrahymena thermophila (SGC5)
49K filament-forming protein
#formal_name Tetrahymena thermophila
14-Oct-1997 #sequence_revision 07-Nov-1997 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. (1997) 237:205-210
Direct demonstration of the bifunctional property of
Tetrahymena 14-nm filament protein/citrate synthase
following expression of the gene in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetrahymena 14-nm filament-forming protein has citrate
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Biochem. Biophys Res Commun (1991) 174:1028-1034
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oxo-acid-lyase
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Biochem. Biophys. Res. Commun. (1997
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##residues 1-462
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##molecule_type DNA
##residues 1-486 ##label WAN
##cross-references EMBL:U31900; NID:g1276597; PID:g939735; MIPS:YPR001w
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##Cross-references EMBL 248951; NID:q762999; PID:q763000; MIPS:YPP001w
##experimental_source strain AB972
**NOE S57724
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Hall, J.; Storms, R.K.; Vo, D.H.; Winnett, E.
submitted to the EMBL Data Library, July 1995
The sequence of Saccharomyces cerevisiae chromosome XVI righ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 VIPKKLLIYKKIANPYPNVDCHSGVLLYSLGLIEYQYYTVVFAVSRALG-CMANLIWSRA 440
                                                                                                                                                                                                                                                                                                              355 VVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGIC-SQLIWDRA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 CLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVIH 234
                                                                       262 CDHEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTK 321
                                                                                                                    235 SDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGFLHGLANQEVLLWIKSVVDECGEN 294
                                                                                                                                                                     322 VSDKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCAD 381
                                                                                                                                                                                                                295 ISTEQLKDYVWKILNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYE 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein LP21w; protein YP9723.01; protein YPR001w
#formal_name Saccharomyces cerevisiae
19-May-1995 #sequence_revision 01-Sep-1995 #text_change
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852814
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submitted to the EMBL Data Library, June 1995
S57724
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NCE
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##residues 1-486 ##label JIA
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Flickinger, M.C.
#journal Appl. Environ. Microbiol. (1992) 58:335-345
#title Cloning and nucleotide sequence of the gene coding for citrate synthase from a thermotolerant Bacillus sp.
#cross-references MUID:92171501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 -LP-D-DPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLF 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 HGGANEAVM----EMLQD-AQTV--EGFKHLLHDKLSKKEKIMGFGHRVYMKKMDPRAAM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 HGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGV-LRKTDPRYTC 331
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143 RKLPHYTEKVLSSLPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDTLEDSL 202
                                        119 S-IPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKG-IHKSKFWEPTYEDCL 176
                                                                                                                                                                     263 LDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQEV 322
                                                                                                                                                                                                                                                           323 VRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLEFAQKR 381
                                                                                                                                                                                                                                                                                                                                             382 PIEFENDKNVLLMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLFFTVIF 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 LLLTGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTELLNREHSTNL-KRAYQ--L-L-GKIPNIVANSYHILHSEEPVQPLQD-LSYSANFLY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 QKAYEKGIHKSKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAH 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A43936 #type complete citrate synthase Bacillus sp. #formal_name Bacillus sp. 10.Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                                            203 NLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNLTSQQS
                                                                                                                                                                                              #superfamily citrate (si)-synthase
#length 373 #molecular-weight 41970 #checksum 2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 323; DB 2; Length 373;
larity 28.9%; Pred. No. 3.51e-37;
Conservative 82; Mismatches 119; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                 442 GCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLEALTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 GVSRSLGICSQLIWDRALGLPLERPKSVTMEWLEKFCK 434
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nes 92; Conser
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SUMMARY
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K.U.; Sahm, H
Microbiology (1994) 140:1817-1828
Nuclectide sequence, expression and transcriptional analysis
of the Corynebacterium glutamicum gltA gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of
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267 GLAGPLHGLANQEVLLMIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 LLINGELPTPDELHKFNDEIRHHTLLDED-FKSOFNVFPRDAHPMATLASSVNILST-Y- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 FQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 RMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ-NCSTSTVRMIGSAQANMFVSIAGGIN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 ALSGPLHGGANQAVLEMLEDIKSNHGGD-ATEFMNK-V-KNKEDGVRLMGFGHRVYKNYD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 LLLTGKVPSKEQVDALSADLRKRASIPDHVYKT-IDALPITAHPMTQFCTGVMALQTRSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 YQDQLN-PLDEAQL-D-K-AT-VRLMAKVPMLAAYAHRAR-KGAPYMYPDNSLNARENFL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 PRAAIVKETAHEILEHLGGDDLLDLAIKL-EEIA-LADDYFISRKLYPNVDFYTGLIYRA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKOPC *type complete citate (si)-synthase (GC 4.1.3.7) - Acetobacter aceti citate (aranal_name Acetobacter aceti 30-Sep-1992 *sequence_revision 30-Sep-1992 *text_change
                                                                                                                                                                                                             #formal_name Corynebacterium glutamicum
16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                            Eikmanns, B.J.; Thum-Schmitz, N.; Eggeling, L.; Luedtke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #active_site His #status predicted
#length 437 #molecular-weight 48929 #checksum 2093
                                                                                                                          140717 *type complete citrate (si)-synthase (EC 4.1.3.7) - Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.0%; Score 324; DB 2; Length 437; Best Local Similarity 28.7%; Pred. No. 2.28e-37; Matches 91; Conservative 94; Mismatches 105; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily citrate (si)-synthase
carbon-carbon lyase; homohexamer; oxo-acid-lyase;
tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      citrate from acetyl-COA and oxaloacetic acid tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ
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##cross-references EMBL:X66112; NID:9505580; PID:9505581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        citrate synthase.
392 YTVLFGVSRSLGICSQLI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 MGFPTD-FFTVLFAIGR 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 YGLTEARYYTVLFGVSR 400
                                                                                                                                                                               glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homohexamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
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#title
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DATE
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Donald, L.J.; Molgat, G.F.; Duckworth, H.W.
J. Bacteriol. (1989) 171:5542-5550
Cloning, sequencing, and:5542-5550
Cloning, sequencing, and expression of the gene for
NADH-sensitive citrate synthase of Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   citrate (si)-synthase (EC 4.1.3.7) - Pseudomonas aeruginosa #formal_name Pseudomonas aeruginosa 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 17-Jul-1998
                                                                      Fukaya, M.; Takemura, H.; Okumura, H.; Kawamura, Y.;
Horinouchi, S.; Beppu, T.
J. Bacteriol. (1990) 172:2096-2104
Cloning of genes responsible for acetic acid resistance in
Acetobacter aceti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 EEVIYLLLNGELPNKVQYDTFTNTLTNHTLLHEQIRNFFNGFRRDAHPMAILCGTVGALS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 EGLLWILLIGKVPSKEQVDALSADLPKPASIPDHVYKTIDALPITAHPMTQFCTGVMALQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 A-F-YPDANDIAIP-AN-RDLA--A-MRLIAKIPTIAAWAYK--YTQGEAFIYPRND-LN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 YAENFLSMMFARMSEPYKVNPVLARAMNRILILHADHEQ-NASTSTVRLAGSTGANPFAC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 YGGNFAHML-G-FDSPQMLE--LMR-LY-VTI-HSDHEGGNVSAHTGHLVGSPLSDPYLS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 IAAGIAALWGPAHGGANEAVLK-MLARIGK-KENIPA-FIAQ-V-KDKNSGVKLMGFGHR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 FAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLG 320
                                                                                                                                                                                                                                                                                                                                                                                 carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis citrate from acetyl-CoA and oxaloacetic acid tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 TRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQV-I-PLDDSLD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 VYKNFDPRAKIMQQTCHEVLTELGIKDDPLLDLAVEL-EKIA-LSDDYFVQRKLYPNVDF 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 VLRKTDPRYTC-QRE-FA-LKHLP--DDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 309; DB 1; Length 436;
Pred. No. 1.45e-34;
85; Mismatches 108; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                *superfamily citrate (si)-synthase allosteric regulation; carbon-carbon lyase; homohexamer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #active_site His #status predicted
#length 436 #molecular-weight 48196 #checksum 9071
                                                                                                                                                                                                                                                        **residues 1-436 **label FUK
**cross-references GB:M34830; NID:q141729; PID:g141730
homohexamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxo-acid-lyase; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 YSGIILKAMGIPTSMF-TVLFAVARTIG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 HSGVLLNHYGLTEARYYTVLFGVSRSLG 403
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**cross-references GB:M29728
homohexamer
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                                                                                                                                                                                                       #cross-references MUID:90202732
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Local Similarity 31.1%;
hes 102; Conservative
17-Jul-1998
                                                                                                                                                                                                                                                  ##molecule_type DNA
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A35157
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borcherl, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brighell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, N.J.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galleron, N.; Ghia,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harmata,
C.R.; Henaut, A.; Hlbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krodh, S.; Kumano, M.;
Maucel, C.; Medique, C.; Medina, N.; Mellado, R.P.; Mixuno,
M.; Mosstl, D.; Nakai, S.; Noback, M.; Nonee, D.; O'Reilly,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.; Perscott,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of citrate from acetyl-CoA and oxaloacetic acid tricarboxylic acid cycle tricarboxylic acid cycle the citrate synthase of gram-negative bacteria is an allosteric enzyme whose activity is inhibited strongly and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 FLHMMFNTPCETKPISPVLAKAMDRIFI-LHADHEQ-NASTSTVRLAGSSGANPFACIAS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 GIAALWGPAHGGANEAVL---R-MLDEIGDVSNIDKFVEKAKDKNDPFKLM-GFGHRVYK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 ALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 LLLTGKVPSKEQVDALSADLRKRASIPDHVYKII-DALPIIAHPMIQFCTGVMALQTRSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 YHDSLD--ITNPKHREVS-AH--RLIAKM?TIAAMVYK--YSKGEPMMYPRND-LNYAEN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 FQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQ-VI-PLDDSLDYGGN 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 KTDPRYTC--QR-EFALKHLP-DDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGV 379
                                                                                                                                                                   specifically by NADH
*superfamily citrate (si)-synthase
allosteric regulation; carbon-carbon lyase; homohexamer;
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citrate synthase III mm90 - Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997 *sequence_revision 05-Dec-1997 *text_change
                                                                                                                                                                                                                                                                                                                                                                                  #length 428 #molecular-weight 47681 #checksum 7548
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.4%; Score 306; DB 1; Length 428; Best Local Similarity 29.3%; Pred. No. 5.24e-34; Matches 95; Conservative 95; Mismatches 98; Indels 36;
                                                                                                                                                                                                                                                                              oxo-acid-lyase; tricarboxylic acid cycle
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Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sekwska, A.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sekwska, A.; Seroc, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Targnoni, M.; Tamakoshi, A.; Tanaka, T.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Vari, A.; Wipat, A.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikawa, H.; Danchin, A. Nature (1997) 300:149-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
#cross-references MUID:98044033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.3%; Score 301; DB 2; Length 372;
Best Local Similarity 28.3%; Pred. No. 4.44e-33;
Matches 96; Conservative 91; Mismatches 124; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #superfamily citrate (si)-synthase
#length 372 #molecular-weight 42106 #checksum 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown; translation not shown
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 16:50:52 1999; MasPar time 13.81 Seconds 894.613 Million cell updates/sec

Run on:

Tabular output not generated.

>US-08-702-718-4 (1-437) from USO8702718.pep 3243 1 SSNLDLRSELQELIPEQQER......LERPKSVIMEWLEKFCKRRA 437 Title:

Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 50.720; Variance 85.362; scale 0.594 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Query	86.9	69.3	64.6	61.5	58.3	57.7		54.8	4		54.3	52.5	44.7	٠.	10.0	•	•	9.3	9.3	•	•	8.5	8.0
Score	2817	2249	2096	1993	1890	1870	1815	1778	1777	1767	1761	1701	1451	1261	323	324	309	301	303	202	288	266	261
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86.9%; Score 2817; DB 1; Length 471;

Query Match

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01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANDOTATION UPDATE)
CITRATE SYWHASE, MITOCHONDRAL PRECUSSOR (EC 4.1.3.7).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
CUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                          121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                  301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
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                                                          35 SADLDLHSQLKEMIPEQQERLKKVKSDLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDP 94
                                                                                               1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP 60
                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "ISOlation of a cDNA encoding mitochondrial citrate synthase Arabidopsis thaliana.";
PLANT MOL. BIOL. 13:411-418(1989).
-:- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O + OXALOACETATE.
Pred. No. 0.00e+00;
42; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METABOLISM. SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
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Best Local Similarity 84.4%;
Matches 369; Conservative
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CISY_ARATH
P20115;
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                                                                                                                                                                                                                                                                                                                                                                                                                             214 LIARVPVVAAYVYRRMYKNGDSIPSDKSLDYGANFSHMLGFDDERLKELMRLTSPSTVMH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                               274 EGGNVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCLTELES-EEPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA 450
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                                                                                                                                                                                                                                                                                                                                   61 EEGIRFRGFSIPECQX-LLPAA-SAGAEPLPEGLL-WLLLTGKVPSKEQVDALSADLRKR 117
                                                                                                                                                                                                                                                                                                                                                                                                 118 ASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 EQLKEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQREFALKHHPDDPLFQ-CCKLMKL-A 391
                                                                                                                                                                                                                                             36 STDLDLKSQLQELIPEHKDRLKKLKSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDP 95
                                                                                                                                                                                                                                                               8; Gaps
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BLOXIAMD D.P., PRINELEE D.C., KUMAR S., WALSH K.A., TITANI K.;

"Complete amino acid sequence of porcine heart citrate synthase.";

BLOCHEMISTRY 21:2028-2036(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVANS C.T., OWENS D.D., SUMEGI B., KISPAL G., SRERE P.A.; *Isolation, nucleotide sequence, and expression of a cDNA encoding
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
HSSP; P23007; SCSC.
LYASE: TRICREDXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                   DB 1; Length 472;
                                                                                                                                                                                                               52; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-UUL-1986 (REL. 01, CREATED)
01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOFATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
', 954AFA81 CRC32;
                                                                                                                                                                                                   Pred. No. 0.00e+00;
                                                                                           CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 AA
                                                                            MITOCHONDRION
                                                                                                                                                                                   Score 2249;
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                                                                                                        309 309 BY
355 355 BY
407 407 BY
472 AA; 52941 MW;
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                                                                                                                                                                                 Query Match
Best Local Similarity 71.7%;
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                                                                                                                                                                                                               314; Conservative
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SUS SCROFA (PIG).
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P00889;
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                                                                                                                                                 SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
              MEDLINE; 83010291.

REMINGTON S, WIEGAND G, HUBER R;
"Crystallographic refinement and atomic models of two different forms of citrate synthase at 2." and 1.7-A resolution.";
J. MOL. BIOL. 158:111-152(1982).
                                                                           MEDLINE; 91104711.
ALTER G.M., CASAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
"Mutation of essential catalytic residues in pig citrate synthase.";
BIOCHEMISTRY 29;7557-75631(1990).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                          PIR, A29966; YKPG.
PDB; ICTS; 16-JUL-88.
PDB; 2CTS; 09-OCT-88.
PDB; 3CTS; 09-OCT-88.
PDB; 4CTS; 16-JUL-88.
PROSTIE: PS00480; CITRATE_SYNTHASE; 1.
PROSTE: PRICARROYXLIG ACID CYCLE: MITOCHONDFION; 3D-STRUCTURE: TRANSIT PEPTIDE; MEHMIATION. 3D-STRUCTURE: TRANSIT PEPTIDE; MEHMIATION.
                                                                                                                                                                            : SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY,
                                                                                                                                                                                                                                                                                                                                                                 CITRATE SYNTHASE. METHYLATION (TRI-).
         X-RAY CRYSTALLOGRAPHY (2.7 AND 1.7 ANGSTROMS)
                                                                                                                                 PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                   EMBL; M21197; G164419; -.
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88 DEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAAL 147
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                                                                                                                                                                                                                                                                                                                                                            208 KLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEG 267
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                                                                                                                                                                                                                                                                                 28 ASSINLKDILADLIPKEQARIKTFRQQHGNTVVGQITVDMMYGGMRGMKGLVYETSVLDP 87
                                                                                                                                                                                                                                                                                              1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP 60
                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                 181 OVPVVAAYVYRRMYKNGQVI-PLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEG
                                                                                                                                                                                                                                                                                                                                                                                      268 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEK
                                                                                                                                                                                                                                                        Score 2096; DB 1; Length 464;
Pred. No. 0.00e+00;
79; Mismatches 84; Indels
                                                                                                                                                                                                                                             51529 MW; 3BC38D25 CRC32;
                                                                                                                                                                                                                                                         64.68;
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Matches 269; Conservative
RPKSMSTDGLIKL 460
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SECUENCE
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CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 91255228.

LIAO D.-I., KARPUSAS M., REMINGTON S.J.;
LIAO D.-I., KARPUSAS M., REMINGTON S.J.;
Ciryatal structure of an open conformation of citrate synthase from chicken heart at 2.8-A resolution.";
BIOCHEMISTRY 30:6031-6036(1991).
-!- CATALYTIC ACTIVITY: CITRAIE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                        TISSUE-HEART MUSCLE;
MADLINE; 90248434.
MARPLINES, 90248434.
"Proposed mechanism for the condensation reaction of citrate
"Proposed mechanism for the condensation reaction of citrate
synthase: 1.9-A structure of the ternary complex with oxaloacetate
and carboxymethyl coenzyme A.";
BIOCHEMISTRY 29:2213-2219(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR PDB; 1CSS; 15-OCT-95.

DR PDB; 1AL6; 24-DEC-97.

DR PDB; 1AMZ; 24-DEC-97.

DR PROSITE; PSO(285; Citzate_synt; 1.

KW LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; 3D-STRUCTURE.

TT ACT_SITE 320 320

T ACT_SITE 375 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METABOLISM.
STATLAPITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
STATLAPITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
STATLABLISHED USING THE SEQUENCE OF PIG CITRATE SYNTHASE AND
MODIFYING IT BASED ON THE OBSERVED ELECTRON DENSITY.
1 CSC; 15-APR-91.
                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF OPEN CONFORMATION
                                                                                                                                       01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL (EC 4.1.3.7).
                                                                                     433 AA
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                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                                                                       PRT;
                                                                    LT 4 STANDARD; E CISY_CHICK STANDARD; E 223007; 01-AUG-1991 (REL. 19, CREATED)
                                                                                                                                                                                                                GALLUS GALLUS (CHICKEN)
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15-OCT-90.
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181 KLPCVAAKIYRNLYRAGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 LLEQGAAANPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGADAS 300
                                                                                                                                                                                                                                                                                                                                                                                                                             61 DEGIRFRGFSIPECOKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAAL 120
                                                                                                                                                                                                                                                                                                                                                                                            1 ASSTNLKDVLAALIPKEQARIKTFRQQHGGTALGQITVDMSYGGMRGMKGLVYETSVLDP 60
                                                                                                                                                                                                                                                                                                                                                                                                            1 SSNLDLPSELQELIPPEQQEPLKKIKKEFGSFQLGNINVDMVLGGMPGMTGLLWETSLLDP 60
                                                                                                                                                                                                                                                                                                                                                       / Match 61.5%; Score 1993; DB 1; Length 433;
Local Similarity 60.5%; Pred. No. 0.00e+00;
nes 259; Conservative 72; Mismatches 96; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                       47373 MW; 6E24FE58 CPC32;
                                                                                                                                                                                                                                                 343
364
372
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                                                                                                                                        SEQUENCE
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSIT PEPTIDE
                                                                                                                                                                                                                     CISY_SCHPO
Q10306;
                                                                                                                                                                                                                                                                                                      SPAC6C3.03
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SEQUENCE
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                                                                                                                                                                                                                                                                                  -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDAIIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM: PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
HYPOTHETICAL PROTEIN: LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 RFRGYSIPECQKLLPRAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWNARADLPTHV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 RFRGFSIPECOKLLPAASAGAEPLPEGLLWLLIGKVPSKEQVDALSADLRKRASIPDHV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 VRMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYEDSMDLLAKLPT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 VAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAELMRLYLVIHSDHEGGNVS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 AHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFNYTEEQLKEW 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 NLKEVLSKKIPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTETSVLDPEEGI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 DLRSELOELIPEQOERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00e+00;
76; Mismatches 99; Indels 3; Gaps
                                                                                                                                                            EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                            01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                             BERKS M., SMITH A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA3A630 CRC32;
                                                       468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S42370; S42370.
WORMPEP; T20G5.2; CE00513.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 58.3%;
l Similarity 58.6%;
252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z30423; G458482; -.
                                                       STANDARD;
                                                                                                                                               CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303
349
349
404
468 AA;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                     STRAIN=BRISTOL N2;
420 RPKSVTME 427
                                                                                                                                                                                                                                                                     OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                           METABOLISM.
                                                    CISY_CAEEL P34575:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                394 GKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARGMGLPLERPK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 FRGYTIPECQKLLPSSPNGKQPLPESLFWLLVTGEIPTLSQVQALSADWAARSQLPKFVE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 AHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDY 303
                                                                                   334 VWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSTLYKITPGILLEQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 LKDRLAELIPEKQAEIKKFRAEHGQDVIGEVTINQMYGGARGVRSLIWEGSVLDPNEGIR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN; LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAJANDREAM M.A., WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
01-00T-1996 (REL. 34, CREATED)
01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-00T-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 18145A7D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972;
DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALS SUBMITTED (FEB-1996) TO EMEL/GENBANK/DDBJ DATA BANKS.
-1- CATALYTIC ACTIVITY: CITRAIE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES; SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; DB 1;
0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00480; CITRATE_SYNTHASE; 1. PFAM; PF00285; citrate_synt; 1. HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
482
319
365
83
420
84
54030 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z69731; E223710; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
365
420
482 AA;
                                                                                                                                                                                                                                                                                                             453 SHSTDGLIKL 462
                                                                                                                                                                                                                                                                                                                                                                      423 SVTMEWLEKF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
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PATHWAY TRICARROXYLIC ACID CYCLE
SURCELLULAR LOCATION MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                ELIDRCPPTLHPMAQFSLAVTALEHDSAFAKAYERGMNKHDYWKYEYEDCMDLIAKTVPI 230
                                                                                                                                                                                                                                                                         291 HIGHLVGSALSSPFLSMAASLNGLAGPLHGLANQEVLNFLITMKKEIGDDLSEETIKSYL 350
                                                                                                                                                                                                                                                                                                                                     245 HTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERHASSELT P , AERT R , VOET M ., VOLCKAERT G , Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FDB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FDB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRALE SYMTHASE, MITCHONDRIAL PRECURSOR (EC 4.1.3.7).
CITI OR LYS6 OR GLU3 OR YNROULC OR N2019.
CITI OR LYS6 OR GLU3 OR YNROULC STANSY.
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                             351 WKLLNSGRVVPGYGHAVLPKTDPRYTAQPEFALEHLPKDPMFQLVSPLYEIVPGVLTEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 KTKNPYPNVDSHSGVLLQYYGLKEQSFYTVLFGVSRTLGVASQLIWDRALGLPIERPKSF
                                                                                                                                    231 AGRIYRNLYRDGVVAPIQMDKDHSYNFANVLGFANNEEFVELMRLYLTIHADHEGGNVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening method EMBO J. 3:1773-1781(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95028151.
LALO D., STETTLER S., MARIOTTE S., GENDREAU E., THURIAUX P.;
"Organization of the centromeric region of chromosome XIV in
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-D273-10B;
LINDNER P., PLUECKTHUN A.;
SUBMITTED (JUL-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUISSA M., SUDA K., SCHATZ G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEAST 10:1355-1361(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST 10:523-533(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-D273-10B;
MEDLINE; 85003587.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 PEHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLLG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 NVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYSKETI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 EEGIRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARSEI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 ASEQTLKEPFAEIIPAKAEEIKKFKKEHGKTVIGEVLI.FQAYGGMRGIKGLVWEGSVLDP 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 KLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDHEGG
                                                                                                                                                                                                                                                                                                                             LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Indels
SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
E -> Q (IN REF. 2).
E -> EE (IN REF. 2).
W; C6896385 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1815; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CISY_EMENI STANDARD; PRT; 474 AA. 000098; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRION
                                                                                                                                                                                                                                                                               PSO0480; CITRATE_SYNTHASE; 1.
00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                   479 C S 312 B B 413 B B 588 E E 78 E 53360 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 56.0%;
Local Similarity 57.1%;
Les 244; Conservative
                                                                                                                                                              EMBL; Z23259; G313750; -.
                                                                                                                                                                                X00782; G3603; -. X77395; G496718; -. Z71616; E239778; -
                                                                                                                                                                                                                             PIR; A01110; YKBY.
PIR; S35390; S35390.
                                                                                                                                                                                                                                                               SGD; L0000341; CIT1
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PFAM; PF00285;
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EMBL; X77395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 KTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIAQVPVV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 AAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGFADNKDFVELMRLYLTIHSDHEGGNVSA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 HTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTEMKKVVGNDLSDQSIKDYL 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 KTKNPYPNVDAHSGVLLQYYGLTERNYYTVLFGVSRALGVLPQLIIDRAFGAPIERPKSF 461
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                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                      "Cloning and characterization of the citA gene encoding the mitochondrial citrate synthase of Aspergillus nidulans."; MOL. CELLS 7:290-295(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1778; DB 1; Length 474; Pred. No. 0.00e+00;
                                                      EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; EMERICELLA.
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                    4.1.3.7).
                                                                                                                                                                                        PARK B.W., HAN K.H., LEE C.Y., LEE C.H., MAENG P.J.;
                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
D97E1E91 CRC32;
                    CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC
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BY SIMILARITY.
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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356
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474 AA;
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                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.00e+00;
74; Mismatches 100; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSHIDA Y., MIYAKE K., KANAYAMA S., KIRIMURA K., USAMI S.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRION (BY SIMILARITY). CITRATE SYNTHASE.
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                                                                                                                                                                                        01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
4; 48D237BC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00285; citrate_synt; 1. HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52153 MW;
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Local Similarity 58.6%;
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                                                                                                                                   STANDARD;
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356 3
411 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WU-2223L;
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425 TME 427
                                                                                                                               CISY_ASPNG
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                                                                                                                                                               P51044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 WSTLNAGOVVPGYGHAVLRKTDPPYVSQREFALRKLPDDPMFKLVSQVYKIAPGVLTEHG 401
                                                                                    92 FRGRTIPDIQKELPKAPGGEEPLPEALFWLLLTGEVPTEAQTRALSEEFAARSALPKHVE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 FRGFSIPECOKLLPAASAGAEPLPEGLLWLLIGKVPSKEQVDALSADLRKRASIPDHVY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 ELIDRSPSHLHPMAQFSIAVTALESESQFAKAYAKGVHKSEYWKYTYEDSIELLAKLPTI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 LKQRLEEILPAKAEEVKQLKKDYGKTVIGEVLLEQAYGGMRGIKGLVWEGSVLDPIEGIR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LRSELQELIPEQQEFLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 55
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                                                                  402 KTKNPYPNVDAHSGVLLQYYGLTEANYYTVLFGVSRALGVLPQLIIDRALGAPIERPKSY
                                                                                                                                                                                                                                                                                                                                                                           FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           UEDA M., SANUKI S., KAWACHI H., SHIMIZU K., ATOMI H., TANAKA A.;
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.
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                                                                                                                                                                                                                                                                     01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNORATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEE342A9 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                        467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB001565; G1871439; -.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                      PRT;
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HSSP; P23007; 5CSC.
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                                                                                                                                                                                                                                                                                                                                                             CANDIDA TROPICALIS (YEAST)
                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            CANDIDACEAE; CANDIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OXALOACETATE
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347
402
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                                                                                                                                                                     425 TME 427
                                                                                                                                     462 STE 464
                                                                                                                                                                                                                                      CISY_CANTR
P79024;
                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- DEVELOPMENTAL STACE: ABUNDANT AFTER 6-12 HRS OF GROWTH. IT IS
NOT SIGNIFICANTLY EXPRESSED AFTER 24 HRS, WHICH IS SEVERAL HRS
AFTER ENTERING THE STATIONARY PHASE OF GROWTH.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                      244 AHIGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLMIKSVVDECGENISTEQLKDY 303
                                                                             272 AHTTHLVGSALSSPFLSLAAGLNGLAGPLHGRANQEVLEWLFKLREELNGDYSKEAIEKY 331
                                                                                                                                                                                           304 VWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLEL 363
                                                                                                                                                                                                                                  392 GMTKNPWPNVGSHSGVLLQYYGLTEESFYTVLFGVSRAFGVLPQLILDRGLGMPIERPKS 451
                                                                                                                                                                                                                                                      212 AAKIYRNVFHDGKLPAQIDSKLDYGANLASLLGFGENKEFLELMRLYLTIHSDHEGGNVS 271
                                                                                                                                                      332 LWDTLNAGRVGPGYGHAVLRKTDPRYTAQREFALKHMPDYELFKLVSNIYEVAPGVFDQH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEREA T., CONTRERAS E.T., OUNG T., BOWMAN E.J., BOWMAN B.J.;
"Characterization of the cit-1 gene from Neurospora crassa encoding
the mitocohondrial form of citrate synthase.";
MOL. GEN. GENET. 242:105-110(1994).
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYASE: TRICARBOXYLIC ACID CYCLE; MITOCHONDRION: TRANSIT PEPTIDE; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
SORDARIALES; SORDARIACEAE; NEUROSPORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
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CITRATE SYNTHASE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                               469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00480; CITRATE_SYNTHASE; 1.
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HSSP; P23007; 5CSC.
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                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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469
352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                             452 FSTE 455
                                                                                                                                                                                                                                                                                                                                                424 VTME 427
                                                                                                                                                                                                                                                                                                                                                                                                                   CISY_NEUCR
P34085:
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SEQUENCE
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Score 1761; DB 1, Length 469,

54.38,

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                     158 ELIDRCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLPTI 217
                                                                                                                                                                                                                                                                                                                                                                                                                         278 HTTHLVGSALSSPFLSVAAGLNGLAGPLHGLANQEVLNWLTEMKKVIGDDLSDEAITKYL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 FRGKTIPECQELLPKAPGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKFIE 157
                                                                                                                                                    6 LRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPEEGIR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mitochondrial and nonmitochondrial citrate synthases in Saccharomyces cerevisiae are encoded by distinct homologous genes."; MOL. CELL. BIOL. 6:4509-4515(1986).
                                                                                                     38 LKERFAELLPENIEKIKALRKEHGSKVVDKVTLDQVYGGARGIKCLVWEGSVLDAEEGIR 97
                                       3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 AARIYQNVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELLRLYLTIHTDHEGGNVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 FRGFSIPECOKLLPAASAGAEPLPEGLLWLLLTGKVPSKEOVDALSADLRKRASIPDHVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 AAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGF-DSPQMLELMRLYVTIHSDHEGGNVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 WDTLNAGRVVPGYAHAVLRKTDPRYSAQRKFAQEHLPEDPMFQLVSQVYKIAPKVLTEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 KTKNPYPNVDAHSGVLLQHYGLTEANYYTVLFGVSRAIGVLPQLIIDRAVGAPIERPKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SYNTHAGE, PEROXISOMAL (EC. 4.1.3.7).
CIT2 OR YCROOSC OR YCRSC OR YCR043.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIAO X., SMALL W.C., SRERE P.A., BUTOW R.A.;
"Intramitochondrial functions regulate nonmitochondrial citrate synthase (CIT2) expression in Saccharomyces cerevisiae.";
MOL. CELL. BIOL. 1:38-46(1991).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BITEAU N., FREMAUX C., HEBRARD S., MENARA A., AIGLE M., CROUZET "The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae."; YEAST 8:61-70(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 87089811.
ROSENKRANTZ M., ALAM T., KIM K.-S., CLARK B.J., SRERE P.A.,
                                    81; Mismatches 103; Indels
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - SUBCELLULAR LOCATION: PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACCHAROMYCETACEAE; SACCHAROMYCES
Best Local Similarity 56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-24 FROM N.A.
                                    245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458 STDKWIE-ICKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 TME-WLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91094853.
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P08679:
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                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
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-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AAKIYRNVFKDGKMGEVDPNADYAKNLVNLIGSKDEDFVDLMRLYLTIHSDHEGGNVSAH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 TKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQLITDRAIGASIERPKSYS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 VKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSOLIWDRALGLPLERPKSVT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 FRGRTIADIQKDLPKAKGSSQPLPEALFWLLLTGEVPTQAQVENLSADLMSRSELPSHVV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 QLLDNLPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSYTFEDSLDLLGKLPVI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 TSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEVLEWLFALKEEVNDDYSKDTIEKYLW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 DILNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHFPDYELFKLVSSIYEVAPGVLTEHGK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 KTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLELGK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 LKERFSEIYPIHAQDVRQFVKEHGKTKISDVLLEQVYGGMRGIPGSVWEGSVLDPEDGIR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                       LYASE, TRICARBOXYLIC ACID CYCLE, PEROXISOME, MULTIGENE FAMILY.

ACT_SITE 293 293 BY SIMILARITY.

ACT_SITE 339 339 BY SIMILARITY.

ACT_SITE 344 394 BY SIMILARITY.

SITE 458 460 MICROBODY TARGETING SIGNAL (POTEN SEQUENCE 460 AA; 51413 MW; 9E9352FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1701; DB 1; Length 460
Pred. No. 0.00e+00;
90; Mismatches 105; Indels
                                   -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REL. 21, CREATED)
(REL. 21, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00342; MICROBODIES_CTER; PROSITE; PS00480; CITRATE_SYNTHASE;
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                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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Similarity 53.8%;
                                                                                                                                                                                                              EMBL; 211113; G3299; -.
EMBL; M14686; G171227; -.
EMBL; M54982; G171229; -.
EMBL; X59720; E264468; -.
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                                                                                                                                                                                                                                                                                                                       SGD; L0000342; CIT2.
                                                                                                                                                                                                                                                                               PIR; A25393; YKBYC.
YEPD; 5440; -.
                    METABOLISM
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01-MAR-1992 (
01-FEB-1994 (
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es 227;
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295 ISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYE 354

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                    CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                    TETRAHYMENA THERMOPHILA.
EUKARYOTA: ALVEOLATA; CILIOPHORA; OLIGOHYMENOPHOREA; HYMENOSTOMATIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 SMDLIAKIPRVAAIIYRHKYRDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECIRGYLSIH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 CDHEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 VSDKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCAD 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 QGIIFRGYTIPQLKEFLPKADPKAADOANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWO 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1451; DB 1; Length 462;
Pred. No. 0.00e+00;
91; Mismatches 124; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQTNLKKVIAEIIPQKQAELKEVKEKYGDKVVGQYTVKQVIGGMRGMKGLMSDLSRCDPY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDPE 61
                                                                                                                                                                                                                          BIOCHEM. BIOPHYS. RES. COMMUN. 174:1028-1034(1991).
-!- FUNCTION: STRUCTURAL PROPEIN INVOIVED IN OPAL MOPPHOGENESIS AND
IN PRONUCLEAR BEHAVIOR DUILING CONJUGATION. RESPIRATORY ENZYME.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL. COA + H(2)O +
                                                                                                                                        NUMATA O., TAKEMASA T., TAKAGI I., HIRONO M., HIRANO H., CKIBA J.,
WATANABE Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 SDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 NRGTVNQDCVNFILNLPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 KRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKG-IHKSKFWEPTYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 CLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIH
                                                                                                                                                                                        "Tetrahymena 14-nm filament-forming protein has citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION MITOCHONDRIAL MATRIX AND CYTOPLASMIC
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
786A39BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION.
                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 22-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D90117; E33571; -.
PIR; JN0130; JN0130.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
HSSP: P23007; SCSC.
                                                                                                                                                                                                                                                                                                                          PATHWAY: TRICARBOXYLIC ACID CYCLE.
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Similarity 48.9%;
                                                                        TETRAHYMENINA; TETRAHYMENA.
                FILAMENT-FORMING PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER
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                                                                                                                                  91128358
                                                                                                                                                                                                                                                                                                                                                                                    CYTOSKELETON.
                                                                                                                                                                                                                                                                                                          OXALOACETATE
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300
346
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SEQUENCE
                                                                                                                                                                                                              activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                    382 VIPKKLLIYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSRA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE 315 BY SIMILARITY.

ACT_SITE 315 BY SIMILARITY.

ACT_SITE 419 HY SIMILARITY.

SITE 419 HY SIMILARITY.

SITE 484 486 MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102; Mismatches 123; Indels 26; Gaps
                                                                                                                                                                                                                                                                                      CISX_TRAST STANDARD; PRT; 486 AA.
P43635;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 35, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEARSON D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METABOLISM.
-!- SIMILAPITY· BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CW04;
JIA Y.K., BECAM A.-M., SLONIMSKI P.P., HERBERT C.J.;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1261; DB 1;
Pred. No. 1.32e-268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   806F987D CRC32;
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PROSITE; PS00342; MICROBODIES_CTER; 1.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N<sub>O</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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                                                                                                                       441 FGLPIERPGSADLKWFHDKY 460
                                                                                                                                                                              414 LGLPLERPKSVTMEWL-EKF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.9%;
Similarity 45.2%;
207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                              203 NLIASLPLITGRIYSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNLTSQQS 262
                                                                                                                                                                                                                                                                                                                                                                                       340 -LP-D-DPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLF 396
                                                                                323 VRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLEFAQKR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                             382 PIEFENDKNVLLMOKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLFFTVIF 441
                                                          83 PEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELAIRG 142
                                                                                                                                   143 RKLPHYTEKVLSSLPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDTLEDSL 202
                                                                                                                                                                                                                                                  177 SLIAQVPVVAAYVYRRMYKNGQVI-PLDDSLDYGGNFAHMLGF----DSP-----QM- 223
                                                                                                                                                                                                                                                                                        LDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQEV 322
                    1 SSNLDLRSELQELIPEQGERLKKIKKEFGS-FQLGNINVDMVLGGMRGMTGLLWETSLLD 59
SCHENDEL F.J., AUGUST P.R., ANDERSON C.R., HANSON R.S., FLICKINGER M.C.; "Cloning and nucleotide sequence of the gene coding for citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase from a thermotolerant Bacillus sp.";
APPL. ENVIRON. MICROBIOL. 58:335-345(1992).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442 GCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLEALTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 GVSRSLGICSQLIWDRALGLPLERPKSVTMEWLEKFCK 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-EDB-1994 (REL. 28, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; Q53554; 1AJ8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A43936; A43936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS COAGULANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-ATCC 55182; MEDLINE; 92171501.
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P27660;
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Score 323; DB 1; Length 373;
Pred. No. 9.74e-44;
82; Mismatches 119; Indels 25; Gaps 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 MLGFDSPOMLELMRL--YVTIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPL 272
                                                                                                                                                                                                                                                                                                                                                                           164 MITGKKPTELEEKIFDRSLVLYSEHFLPN-STFTARVIASTLSDLYGALTGAVASLKGHL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 HGGANEAVM----EMLQD-AQTV--EGFKHLLHDKLSKKEKIMGFGHRVYMKKMDPRAAM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 HGLANQEVLLMIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGV-LRKIDPRYIC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 OREFALKHLPDDDFFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARY 391
                                                                                                                                                                                                                                                                                          95 LLLTGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEF 154
                                                                                                                                                                                                                                                                                                                                               110 DTELLNREHSTNL-KRAYQ--L-L-GKIPNIVANSYHILHSEEPVQPLQD-LSYSANFLY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 MKE-ALKELSAVNGDDLLLQMCEAGEQIMRE--E-KGLFPNLDYYAAPVYWKLGIPIPLY 331
LYASE, TRICARBOXYLIC ACID CYCLE; ALLOSTERIC ENZYME.
ACT_SITE 252 262 BY SIMILARITY.
ACT_SITE 314 BY SIMILARITY.
SEQUENCE 373 AA; 41970 MW; 8C8B68C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: Fri Oct 22 16:51:58 1999 Job time : 66 secs.
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                                                                                                                                Match 10.0%;
Local Similarity 28.9%;
les 92; Conservative
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Best Local S
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Run on:

Fri Oct 22 16:52:16 1999; MasPar time 27.64 Seconds 863.073 Million cell updates/sec

Tabular output not generated.

>US-08-702-718-4 (1-437) from USO8702718.pep 3243 1 SSNLDLRSELQELIPEQQER......LERPKSVTMEWLEKFCKRRA 437 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organolle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 48.796; Variance 86.952; scale 0.561 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

SUMMARIES	ength DB ID Description Pred. No	10 Q96544 CITRATE (SI)-SYNTHASE 0.	474 10 064869 CITRATE SINTHASE (EC 4 0.00E+00	10 024135 CITRATE SYNTHASE (EC 4	0	10	466 4 075390 CITRATE SYNTHASE (EC 4 0.00e+00	372 1 028929 CITRATE SYNTHASE (CITZ 8.07e-31	_	2 O68883 CITRATE SYNTHASE (EC 4 1	431 2 033066 CITRATE SYNTHASE (EC 4 7.59e-25	2 034002 CITRATE SYNTHASE. 1	2 Q53115 CITRATE SYNTHASE (FRAG 4.	356 2 054382 CITRATE SYNTHASE (EC 4 1.55e-21	7				411 2 P77936 CITRATE SYNTHASE (EC 4 9.10e-21	
	lptic				)LAM					-	-				-					
	Descr	CITRA	CITRA	CITRA	ETHAN	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA	CITRA
SUMMARIES	qi	096544	064869	024135	043175	024259	075390	028929	032705	068883	033066	034002	053115	054382	059777	059775	060047	059779	P77936	059469
		10	10	10			4	П	-	7	7									
	% Query Match Length	437	474	469	471	339	466	372	379	427	431	379	411	326	411	411	411	411	411	411
	% Query Match	100.0	87.4	86.3	81.3	66.8	63.8	8.3	7.9	7.4	7.4	7 0	7.0	•	6.9	6.8			6.8	6.7
	Score	3243	2834	2800	2637	2166	2072	270	256	239	240	228			223			219		218
	Result No.	10	4 M	4	2	9	7	σ	0	10	11	12	13	14	15	16	17	18	19	50

21 212 6.5 429 2 033915 CITRATE SYNTHASE (EC 4 2 2 2007 6.4 410 2 059769 CITRATE SYNTHASE (EC 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
2 207 6.5 429 2 03391 2 207 6.4 410 2 05976 2 207 6.4 410 2 05976 179 5.5 399 2 07000 158 4.9 315 2 05923 158 4.9 318 2 05923 158 4.9 318 2 05923 158 4.9 318 2 05923 158 4.9 319 2 07082 145 4.6 321 2 05923 144 4.5 319 2 07082 144 4.5 319 2 07082 144 4.5 319 2 07082 144 4.5 319 2 07082 100 3.1 295 2 06614 101 3.2 299 2 04554 101 3.1 522 5 02328 102 3.1 522 5 02328 103 3.1 522 5 02328 104 3.1 522 5 02328 105 3.1 738 5 03355 107 3.1 738 5 03357 108 3.1 738 5 03357 109 3.1 738 5 03357
22 207 6.5 429 2 200 6.4 410 2 200 6.2 410 6 4 410 6 5 6 7 410 7 158 4.9 315 1 188 158 4.9 318 8 158 4.9 318 1 145 4.6 321 1 145 4.6 321 1 145 4.5 319 1 104 3.2 294 1 100 3.1 229 1 100 3.1 522 1 100 3.1 738 2 102 3.1 1229 2 102 3.1 1229 2 102 3.1 1229 2 102 3.1 1229
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## ALIGNMENTS

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301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 PEHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKTKYWEPTYEDSITLIA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 QLPVVAAYIYRRMYKNGQSISTDDSLDYGANFAHMLGYDSPSMQELMRLYVTIHTDHEGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVSECGENVTKEQL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                             241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                                                                                                      301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFGLVSKLYEVVPPIL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 ASDLDLRSQLKELIPEQQERIKKLKAEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; ARALIALES; APIACEAE; DAUCUS.
                                                                                                                                                                                                                            181 QVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEGG
                                                                                                                                                                                                          361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-i- CITPATE SYNTHASE IS FOUND IN NEAPLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.4%; Score 2867; DB 10; Length 472; 85.4%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. MS YONSUN;
TAKITA E., KOYAMA H., SHIRANO Y., SHIBATA D., HARA T.;
"CDNA encoding carrot mitochondrial citrate synthase.";
SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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EMBL: AB017159; D1033521; -.
LPAGSITE; PS00480; CITRATE_SYNTHASE; 1.
LPAGSE; TRICARBOXYLIC ACID CYCLE.
SEQUENCE 472 AA; 52656 MW; D46C38CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITRATE SYNTHASE (EC 4.1.3.7)
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Matches 373; Conservative
                                                                                                                                                                                                                                                                                   421 PKSVTMEWLEKFCKRRA 437
                                                                                                                                                                                                                                                                                                                       421 PKSVTMEWLEKFCKRRA 437
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                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 KEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQREFALKHLPDDPLFQLVSKLYEVVPPVL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 TELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLALER 455
                                                                                   396 TELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRAIGICSQLVWDRALGLPLER 455
                                                                                                                            361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 EEGIRFRGLSIPECQKVLPTAQSGAEPLPEGLLWLLTGKVPSKEQVEALSKDLANRAAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 PDYVYNAIDALPSTAHPMTQFASGVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 NVSAHTGHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQL 335
336 KDYIWKTLNSGKVVPGYGHGVLRNTDPRYICQREFALKHLPDDPLFQLVSNLFEVVPPIL 395
                                      301 KDYVWKILNSGKVVPGFGLGVLRKIDPRYICQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 STDLDLKSQLQELIPEQQDRLKKLKSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; SIREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.,
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
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-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 474;
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39; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
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EMBL; AC004521; G3128180; -.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
LYASE; TRCARBOXLIC ACID CYCLE.
SEQUENCE 474 AA; 52782 MW; 64FF2AC6 CRC32;
                                                                                                                                                                                                                                                                                                       474 AA
                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQ)
01-AUG-1998 (TREMBLREL. 07, LAST ANN
                                                                                                                                                                                                                                                                                                    PRT;
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Best Local Similarity 85.3%;
Matches 371; Conservative
                                                                                                                                                                       456 PKSVTMEWLENHCKKSS 472
                                                                                                                                                                                                                421 PKSVTMEWLEKFCKRRA 437
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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361 LELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRALGLPLER 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 PDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 KDYVWKTLNSGKVVPGFGLGVLRKIDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                               NICOTIANA TABACUM (COMMON TOBACCO).
EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA; EMBRYOPHYTA; FUPHYLES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE: SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 QVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLER
                                                                                                                                                                                                                                                        STRAIN-CV. SNN;
LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER B.;
PLANT CELL PHYSIOL. 0:0-0(0).
-'- CATALYTIC ACTIVITY: CITPATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFL
                                                                                                                                                                                                                                                                                                                                    OF
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 469;
                                                                                                                                                                                                                                                                                                                                -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Mismatches 27; Indels
                                                                                                                    01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2800; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                           PFAM: PF00285; citrate_synt; 1.
LYASE; TRICARBOXXLIC ACID CYCLE.
SEQUENCE 469 AA; 52492 MW; 6BE3C325 CRC32;
                                                                                                469 AA
                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; X84226; E137432; -.
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                       PATHWAY: TRICARBOXYLIC ACID CYCLE
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 86.3%;
Best Local Similarity 85.7%;
Matches 373; Conservative
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PKSVIMEWLEKFCKR 435
                       456 PKSVTMDWLEAHCKK 470
                                              421 PKSVTMEWLEKFCKR 435
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                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                  LT 4
024135
024135;
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120 IPDHV-YKTIDALPITAHPMIQFCTGVWALQIRSEFQKAYEKGIHKSKFWEPIYEDCLSL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 PDEGIRFRGLSIPECOKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEOVNSIVSGIAESGI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 EQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 SSGLDLRSELVQELIPEQQDRLKKIKSDMKG-SIGNITVDMYLGGMRGMTGLLWKPHYLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                     EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 ISLIIMYTTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 LFLONLAKLK-PWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 IAQVPLVAAYVYRRMYKNGDTIPKDESLDYGANFAHMLGFSSSEMHELLMRLYVTIHSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2637; DB 10; Length 4
Pred. No. 0.00e+00;
41; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O24259
O24259:
O24259:
O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-OVV-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
CITRATE (SI)-SYNTHASE (EC 4.1.3.7) (CONDENSING ENZYME)
(CITRATE CONDENSING ENZYME) (CITRAGECONDENSING ENZYME)
(OXALOACETATE TRANSACETASE).
                                            ETHANOLAMINE AMMONIA-LYSSE (TREMENCE OF LAST SEQUENCE UPDATE)
SCHANCHAINE AMMONIA-LYSSE (EC 4.3.1.7).
EURARYOTA, VIRIDIDIANATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 471 AA; 52612 MW; BC96A65C CRC32;
                     471
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.3%;
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 LERPKSVTMEWLENQCKK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-CV. DESIREE; MEDLINE; 96073431.
LT 5
Q43175
Q43175;
01-NOV-1996 (
01-NOV-1996 (
01-JAN-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYASE.
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          POPULUS DELICIDES X POPULUS BALSAMIFERA SUBSP. TRICHOCARPA.
EUKARYOTA: VIPTUPLPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
VIOLALES; SALICACEAE; POPULUS.
                                                                                                                                                                                                                                                                                                                                                         280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPMNDSLVIGGNFSHMLGFDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         161 GIHKSKFWEPTYEDCLSLIAQVPVVAAYVYRRMYKNGQVIPLDDSLDYGGNFAHMLGFDS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEMQELMRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LLWIKSVVEEGGENITTEQUKDYVWKTLNSGKVVPGFGHGVLPKTVPPYTCQPEFALKHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 LLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 PDDPLFQLVSKLYEVVPPVLTQLGKVKNPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSR 300
                                                                                                                                                                                                                                                                                                                                         1 MPTKEQVGALSKELRDRALVHDYVFKAIDALPVTAHPMTQFATGVMALQVQSEFQKAYEK 60
                                                                                                                                                                                                                                                                                                       Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequence analysis of human citrate synthase cDNA."; SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                              LA COGNATA U., LANDSCHUETZE V , WILLMITZER L., MUELLER-POERER PLANT CELL PHYSIOL. 0.0-0.0(0)
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
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0
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-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                   n 66.8%; Score 2166; DB 10; Length 339;
Similarity 85.4%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                       29; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C0532604 CRC32;
                                                                                                                                                                                                                                   SEQUENCE 339 AA; 37834 MW; B2DA24A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 SIGICSQLIWDRALGLPLERPKSVTMELLENHCKK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 SLGICSQLIWDRALGLPLERPKSVTMEWLEKFCKR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - 1 - SIMILARITY - TO OTHER CITRATE SYNTHASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF047042; G3288815; -. PROSITE; PS00480; CITRATE_SYNTHASE; 1. LYASE, TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLREL. 08, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                EMBL, X84227, E276838; -. PFAM; PF00285; citrate_synt; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51706 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                       286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                   OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOLDENTHAL M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LISSUE-HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA;
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                       Local
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075390
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                                                                                                                                                                                                                   LYASE.
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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DB 4; Length 466;

63.9%; Score 2072;

Query Match

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88 DEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRAAL 147
                                                                                                                                                                                                61 EEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKFQVDALSADLPKRASI 120
                                                                                                                                                                                                                                            148 FSHVVIMLDNFPINLHFMSQLSAAVTALNSESNFAQAYARGISFTKYWELIYEDSVDLIA 207
                                                                                                                                                                                                                                                                                     121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                           181 QVPVVAAYVYRRMYKNGQVI-PLDDSLDYGGNFAHMLGFDSPQMLELMRLYVTIHSDHEG 239
                                                                                                                                                                                                                                                                                                                                                                                                                       268 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 LRDYIWNTLNSGRVVPGYGHAVLRKIDPRYTCQREFALKHLPNDPMFKLVAQLYKIVPNV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 LLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYTTVLFGVSRALGVLAQLIWSRALGFPLE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLEKK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
KETCHUM KA., DODSON R.J., CMINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KEPLANGE A.R., GRAHAM D.E., KYPPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
PETERSON S., PEICH C I. MCNEIL L.K., RADGER J.H., GLOBEK A., ZHOIL LOYERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOM P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                28 ASSTNLKDILADLIPKEQARIKTFRQQHGKTVVGQITVDMMYGGMRGMKGLVYFTSVLDP 87
Pred. No. 0.00e+00;
75; Mismatches 90; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 GNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEO
                                                                                                          1 SSNLDLRSELQELIPEQQERLKKIKKEFGSFQLGNINVDMVLGGMRGMTGLLWETSLLDP
                                                                                                                                                                                                                                                                                                                                    208 KLPCVAAKIYRNLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCHAEOGLOBUS FULGIDUS.
ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.3%; Score 270; DB 1; Length 372; Best Local Similarity 27.2%; Pred. No. 8.07e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sulphate_reducing archaeon Archaeoglobus fulgidus."; NATURE 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42270 MW; DB9662BC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-VC-16 / DSM 4304 / AICC 49558;
MEDLINE; 98049343.
KLENK H.-P., CLAYTON R.A., TOMB J -F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00285; citrate_synt; 1.
Best Local Similarity 62.1%;
Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 RPKSVTMEWLEKFCKRRA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001011; G2649234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AA;
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028929
028929;
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387 TEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKS 423

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Query Match 7.9%; Score 256; DB 1; Length 379;
Best Local Similarity 28.2%; Pred. No. 5.18e-28;
Matches 95; Conservative 78; Mismatches 142; Indels 22; Gaps 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GGNFAHMLGFDSP-QML-ELMRLYVI1HSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 AANFLYMLHGEEPTKTAERALDMDLILHAEHEL-NASTFAARIAASTLADIYACVVAATG 212
                                                                                                                                                                                                                                                     209 GGNFAHML-GFDSPQMLE-LMRLYVIIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALN 266
                                                                                                                                                                                                                                                                                               213 TLMGPLHGGAAQEVM---R-MLREVASPRRAE---EYVKRKIEAGERIMGFGHRVYRGVM 265
                                                                                                                                                                                                                                                                                                                                                                                 266 DPRAELLR-YLAKRLAAEG----STKWFEISEAIAKAAYKYKKLLPNVDFYSASVYANLG 320
                                                                                                                                                                                                                                                                                                                                                                                                            326 DPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 EEVLYLLWHGALPTGEELDAFSDELAAHRDLDDGVLDVARELAEQDESPMAALRTLVSAM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 EGLLWLLLTGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAH-PMTQFCTGVMAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 SAYDESA-DFE-DV-TDR--EVNLEKAKRITAKMPSVLA-AYARFRRGDDYVEPDESLNH 159
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                                                                             90 EGLLWLLLTGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMTQFCTGVMALQ 149
                                                                                                                        97 TATSYLGSLDKKIA-VRTREETFNKAKDLIAKFPTIVAY-YHRI-RTGRNIIPPALEFSH 153
                                     44 EEVAYLLIYGELPKKYELQDFKIELAERRELPPQI---1-GL-LT-H-LPPYTHPMVVLR 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARCHAEA; EURYARCHAEOTA; HALOBACTERIALES; HALOBACTERIACEAE; HALOFERAX
87; Mismatches 130; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                       267 GLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLNSCKVVPGFGLGVLKK?-
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MADDOCKS D.G., CONNARIS H., HOUCH D.W., DANSON M.J.;
SUMITIED (COT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJO02075; E1154178; -.
PFAM; PF00285; citrate_synt; 1.
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01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRALE SYNTHASE (EC 41.3 7) (FRAGMENT).
HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 AA; 41848 MW; 480EAC2F CRC32;
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92; Conservative
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01-JAN-1998 (TREMBLREL.
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89 ILLYGEKPTQEEYDEFRITVIRHTMIHEQIIRLFHAFRRDSHPMAVMC-GITGALA-AFY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 LNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQLKDYVWKTLN-SGKV-VPGFGLGVL 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 KNYDPRATVMRETCHEVLKELGTKDDLLEVAMELEHIALNDPYFIEK-K-LYPNVDFYSG 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .Match 7.4%; Score 239; DB 2; Length 427; Local Similarity 27.1%; Pred. No. 1.19e-24; es 88; Conservative 96; Mismatches 103; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYCOBACTERIUM LEPRAE.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HORSWILL A.R., DUDDING A.R., ESCALANTE-SEMERENA J.C.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
GLTA.
                                                                                                       (TREMBLREL. 07, CREATED)
(TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL. AF056043; G3025888; -.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
LYASE; TRACARBOXYLIC ACID CYCLE.
SEQUENCE 427 AA; 48106 MW; F5AB9869 CRC32;
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                                                                                                                                                                                                               CITRATE SYNTHASE (EC 4.1.3.7).
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                                        PRELIMINARY;
                                                                                                       01-AUG-1998 (TREMBLREL. 01-AUG-1998 (TREMBLREL.
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379 AA; 41832 MW; 47DB0E16 CRC32;

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"Sequencing and expression of the gene encoding a cold-active citrate synthase from an Antarctic bacterium, strain DS2-3R.";
EUR. J. BIOCHEM. 248149-57(1997).
PEMBL: U89944; G2431774;
PFAM: PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 M---L-G--FDS-PQML-ELMRLYVTIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 ALWGPLHGGANQAVLEMLEGIR-ESGDDVGG-FVQK-VKNCCAGVKLM-GFGHRVYKNYD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 LLIYGELPATDQLAEFTHRIQRHTMLHEDLKRFYDGFPRNAHPMPVLSSVVNAL-S-AYY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 QDALD-PMDNGQV-ELS--T-IRLLAKLPTIAAYAYKKSVGQPFLYP-DNAFSLVENFLR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 MTFGLPAEPYEPDPEVVRALDMLFI-LHADHEQ-NCSTSTVRLVGSSRANLFTSISGGIN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 GLAGPLHGLANOEVLLWIKSVVDECGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 PRARIVKEQADKILVKLGGDDDLLNIAKGL-EE-AALTDDYFIERKLYPNVDFYTGLIYR 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 LLLIGKVPSKEQVDALSADLRKRASIPDHVYKTIDALPITAHPMTQFCTGVMALQTRSEF 154
                                                                                                                                                                                             EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.; "Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                                                                                                                                                                                                                           -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                               of Mycobacterium leprae.";

WOL. MICROBIOL. 7:197-206(1993).

-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 431;
                                                                       B.G., RAJANDREAM M.A.;
TO EMBL/GENBANK/DDBJ DATA BANKS
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 240; DB 2;
Pred. No. 7.59e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_Synt, 1.
PFASE; TRCARBOXYLIC ACID CYCLE.
SEQUENCE 431 AA; 48111 MW; ICFA87BB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                OXIDATIVE METABOLISM.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL: 299494; E350411; -.
                                                                                                                                                                                                                                                                                                                                                 .! - PATHWAY: TRICARBOXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPEATED)
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05,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 HYGLTEARYYTVLFGVSR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.4%;
Best Local Similarity 27.7%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 ALGFP-TRMFIVLFALGR 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTARCTIC BACTERIUM DS2-3R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLREL
01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                    PARKHILL J., BARRELL SUBMITTED (SEP-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97454284.
                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                           MEDLINE; 93188700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                           OXALOACETATE
                                                                                                                                                                                                                                                                         MOL. MICROBIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-DS2-3R
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034002
  RRERESERVE REPRESERVE 
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Gaps 11;
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                                                                                                                                                                                  227 MRLYVTIHSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKS 286
                                                                                                                                                                                                                                                                                                                                                                                                              236 IGIRKDESLDEAATRSKAWMVDALAQKKKVMGFGHRVYKNGDSRVPTMKS-ALDAMIKHY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 DRPEMIG-LYNGLEAAMEEAKQIK---PNLDYPAGPTYNLMGF-DTEMFTPLFIAARITG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 PFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 KYKVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACVSTGIASLWGPAHGG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 ANEAVINMLKEIGSSENIPKYIAKAKDKNDPFRLMGFGHRVYKNYDL---RAAVLKETCK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ANQEVLLWIKSV--VDECGENISTEQLKDYVWKTLNSG-KVVPGFGLGVLRKTDPRYTCQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 REF-ALKHLPDDPFFQLVSKLYEVVPPILLELGKVKNPWPNVDAHSGVLLNHYGLTEARY 391
                                                                                                                                       118 EANLEKAMSLLATFPSVVAYDQRRR-RGEELIEPREDLDYSANFLWMTFGEEAAPEVVEA 176
                                                                                                                                                                                                                                                                           177 FNVSMILYAEH-SFNASTFTARVITSTLADLHSAVTGAIGALKGPLHGGANEAVMHTFEE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 NFKEADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNALDFTENFLHMM-FATPCE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 EVLKELGQLDGNPLLQIAIEL-EAIA-LKDEYFIERKLYPNVDFYSGIIYKAMGIP-SQM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 M--LE-LMR--LY-VTI-HSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGL
                                                                   69; Mismatches 106; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES.
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
/ Match 7.0%; Score 228; DB 2; Length 379; Local Similarity 26.7%; Pred. No. 1.67e-22; les 69; Conservative 69; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 7.0%; Score 226; DB 2; Length 411; Local Similarity 28.6%; Pred. No. 4.08e-22; es 72; Conservative 70; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-AB BACTERIUM;
SATRAIN-AB BACTERIUM;
SATRAIN-BENCH BACTERIUM;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U59712; G1390003; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 AA; 46189 MW; 9CCB3291 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 WIAHIM-EQVADNALIRP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 ICSQLIWDRALGLPLERP 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITRATE SYNTHASE (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RICKETTSIA SP
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6.9%; Score 223; DB 2; Length 356;
28.7%; Pred. No. 1.55e-21;
Ative 69; Mismatches 86; Indels 24; Gaps 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 --LE-LMR--LY-VII-HSDHEGGNVSAHIGHLVGSPLSDPYLLSFAAALNGLAGPLHGLA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 FKEADYELTAIRMIAKIPTIAAMSYK--YSIGQPFVYPDNSLDFTENFLHMM-FATPCEK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 FWEPTYE-DCLSLIAQVPVVAAYVYRRMYKNGQVIPL-DDSLDYGGNFAHMLGFDSP-QM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 YKVNPVVKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACVSTGIASLWGPAHGGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 NEAVINMLKDIGSVENIPKYIAKAKDKNDNFRLMGFGHRVYKNYD-P--RAAVLKETCKE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 NQEVLLWIKSV--VDECGENISTEQLKDYVWKTLNSG-KVVPGFGLGVLRKTDPRYTCQR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 VLKELGQLDNNPLLQIAIEL-EAIA-LKDEYFIERKLYPNVDFYSGIIYKAMGIP-PQMF 337
                                                                                                                                                                                                                                                             DAVIS M.J., YING Z., BRUNNER B.R., PANTOJA A., FERWERDA F.H.;
"Rickettsial relative associated with papaya bunchy top disease.";
CURR. MICROBIOL. 36:80-84(1998).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                 -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
-:- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL. 1076908, G2894797; -.
EMBL. 1076908. CITRATE SYNTHASE; 1.
EMBL. TRICARBOXYLIC ACID CYCLE.
                                                                                                                                      RICKETTSIA SP.
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HA-91;
RACULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                 01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 AA; 40030 MW; 15BF55D0 CRC32;
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                    356 AA
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                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 28.7%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 TVLFATARTVG 348
                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-PUERTO RICO; MEDLINE; 98087556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Q59777
Q59777;
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LT 14
054382
054382;
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                                                                                                                                                                                                                                                                                                                                               207 KYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTGIASLWGPAHGG 265
                                                                                                                                                                                                                                                                                                                                                                  222 Q-MLE-LMR--LY-VTI-HSDHEGGNVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 ANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRVYKNYD-P--RAAVLKETCK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                            276 ANQEVILMIKSV-VDEC-GENISTEQIKDYVWKTLNSG-KVVPGFGLGVLRKTDPRYTCQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 EVLKELGQLDNNPLLQIAIEL-EAIA-LKDEYFIERKLYPNVDFYSGIIYKAMGIP-SQM 379
                                                                                                                                                                                                                   Query Match 6.9%; Score 223; DB 2; Length 411;
Best Local Similarity 29.0%; Pred. No. 1.55e-21;
Matches 73; Conservative 67; Mismatches 88; Indels 24; Gaps
              OXIDATIVE METABOLISM.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                       411 411
411 AA; 46162 MW; 9921533A CRC32;
                                                        380 FTVLFAIARTVG 391
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392 YTVLFGVSRSLG 403
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Search completed: Fri Oct 22 16:54:47 1999 Job time : 151 secs.


.94e-63 .94e-63 .88e-57

Yeast gene for citrate S.cerevisiae chromosom S.cerevisiae N2019, N2 Candida tropicalis DNA

SCCS01 SCYNRO01C SCN201952 AB001565 SPAC6C3

13e-45 1.04e-39 1.04e-39 1.05e-33 1.05e-33 1.05e-21 1.05e-17 1.05e-17 1.05e-17 1.05e-17 1.06e-07 1.06e-07 1.06e-07 1.06e-05 
Caenorhabditis elegans Arabidopsis thaliana c Emericella nidulans ci

S.cerevisiae citrate s S.cerevisiae chromosom S.cerevisiae chromosom Saccharomyces cerevisi S.cerevisiae chromosom Sequence 14 from paten Sequence 17 from paten Sequence 17 from paten Soleracea L. mRNA for P.falciparum mRNA for Mus musculus transcrip

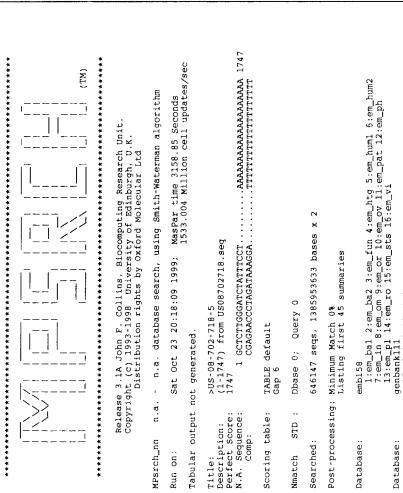
SCCIT3SYN SC9723 SCC131900 SCCHRXVI 166494 A5214 A5214 SOPULSPO PFGTUB AFULSPO PFGTUB AFULSPO AC004153

Drosophila melanogaste Plasmodium falciparum B.verrucosa Betv III m Dictyostelium discoide Dictyostelium discoide

BVBETVIII DDU73686 AB009080

S.pombe chromosome I cast Veast (S.cerevisiae) C S.cerevisiae) C S.cerevisiae) C Aspergilus niger mRNA N.crassa mitochondial Kluyveromyces lactis D I thermophila mRNA fo Caenorhabditis elegans human STS WI-12459.

YSCCIT2
ASNCIT1
NEUCITIA
NEUCITIA
TETCITSY
CET20G5
G13212
CET70G10
ATACO04521
ENU89675



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/translation="MVFYRGVSLLSKLRSRAVQQTNLSNSVRWLQVQTSSGLDLRSEL
                                                                                                                                                                           Nicotiana tabacum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1747)

Pueller-Roeber, B., Landschuetze, V. and La, C.U.

PROCESSES FOR INHIBITING AND FOR INDUCING FLOWEP FORMATION IN

PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Nicotiana tabacum"
/db_wreff"taxon:4097"
/tissue_type-"LEAF"
/clone-"TCS"
                                                                                                                                                                                                                                                                                                                                                    Patent: WO 9524487-A 3 14-SEP-1995;
HOEATHST SCHENICA GREEVO GMBH (DE)
Other publication DE 4435366 960425
Other publication DE 4435366 960328
Other publication AU 2067995 950925
Other publication DE 4408629 950914.
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                  A46547 1747 bp DNA
Sequence 3 from Patent W09524487.
A46547 4547.
A46547.1 GI:2300711
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/EC_number="4.1.3.7"
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                                                                                                                                                           common tobacco.
RESULT 1
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717:95 bal 18:9b ba2 19:9b htg1 20:9b htg2 21:9b in1 22:9b\_in2 23:9b\_om 24:9b\_ov 25:9b\_pat 26:9b\_ph 27:9b\_pl1 28:9b\_pl2 29:9b\_pr1 30:9b\_pr2 31:9b\_pr3 32:9b\_ro 33:9b\_st 34:9b\_sts 35:9b\_sy 36:9b\_un 37:9b\_vi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mean 12.066; Variance 12.847; scale 0.939

Statistics:

0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 2.29e-268 2.29e-268 2.29e-268 3.18e-216 3.18e-216 3.77e-88

Sequence 2 from Patent B.vulgaris mRNA for ci Arabidopsis thaliana m Populus hybrid mRNA fo Homo sapiens citrate s

BVCITSYNH ATMTCITRN PHCITSYNH

100.0 70.9 70.9 70.9 70.9 48.5 48.5 441.6 441.6 441.6 411.6 115.7

1238 1238 1238 1238 1238 1238 1238 1256 1256 1274 1210

1747 1891 1891 1733 1733 1551 1551 1378

Porcine citrate syntha S. cerevisiae mitochond

AF047042 PIGCITSYN SCMTCISNA

1401 1455 1481

Sequence 3 from Patent N. tabacum mRNA for cit Sequence 1 from Patent S. tuberosum mRNA for m Daucus carota mRNA for Citrus maxima citrate

A46547 NTCITSYNH A46545

STCITS AB017159 CMU19481 A46546

Description

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Query Match Length DB

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                             GCTCACACAGGTCACTTGGTTGCTAGTGCTTTGTCAGACCCTTACCTCTTCGCTGCT
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
I (bases 1 to 1747)
La Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B. Plant Cell Physiol. In press
Z (bases 1 to 1747)
La Cognata,U.
Direct Submission
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VAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGGNV
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                                                                                                                                                      Submitted (23-JAN-1995) U. La Cognata,
Genbiologische Forschung, Berlin GmbH,
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1561 AGCCAAGGTAGGTCGCATTAGGATGTTCATCGATTGGCTTAGTACGGTTTTGAAAGATTT 1620
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                                                                                   1621 TGGTTGTGTATTTTCAGTTTCGGTTTTAAAAATGTTATACCAATACCTTATCGATATAAA 1680
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Mueller-Roeber.B., Landschuetze,V. and La,C.U.
PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION IN
PLANTS
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HOECHST SCHERING AGREVO GMBH (DE)
Other publication DE 4438821 960425
Other publication DE 4435366 960328
Other publication AU 2067995 950925
Other publication DE 4408629 950914.
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Submitted (20-SEP-1993) V. Landschuetze, Inst. fuer Genbiologische Forschung, Berlin GmbH, Ihnestr. 63, 14195 Berlin, FRG
2 (bases 1 to 1891)
Landschutze, V., Muller-Rober, B. and Willmitzer, L.
Mitochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds
Planta 196 (4), 756-764 (1995)
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S.tuberosum mRNA for mitochondrial citrate-synthase.
X75082
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/note="ethanolamine ammonia-lyase"
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/organism≈"Solanum tuberosum"
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/db_xref="taxon:4113"
/dev_stage-"mature"
/clone_lib="leaf library"
/clone="5-25-10"
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/db_xref="PID:9483510"
/db_xref="GI:483510"
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LEPEQQVLDAARPGGEPLPEGLIMLILTGKVPSREQVVSTYSGIASSGIISLIIMY
ITIDALPYTAHPWTOFATGWALDYQSEFQRAYEKGIHKSKYWEPTYEDSMNLIAQVP
LVAAYVYRRMYRNGDTIPKDESLDYGANFAHMIGFSSSEMHELLMRLYYIHSPHEGG
                                                                                                      NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLMIKSVVEEGGENISKE
CALDYVWKILLINSGKVYPGFGHGVLRKTVPRYTCQREFAMKHLPEDPLEQLVSKLYEVF
LLELQULLAKLRWPWDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALG
LPLERPKSVTMEWLENQCKKA"
translation="MVFYRSVSLLSKLRSRAVQQSNVSNSVRWLQVQTSSGLDLRSEL"
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                                                                                                                                                                                                                                                                                                           Indels 18;
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Pred. No. 0.00e+00;
0; Mismatches 93; Indels 18;
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Best Local Similarity 92.8%;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudlcotyledons; Asteridae; Aralhales; Aplaceae; Daucus.

1 (bases 1 to 1859)
Takita,E., Koyama,H., Shirano,Y., Shibata,D. and Hara,T.
Sirect Submission
Trakita,E., Koyama,H., Shirano,Y., Shibata,D. and Hara,T.
Submisted (26-AUG-1998) to the DDBJ/EMBL/GenBank databases. Eiji
Takita, Gifu University, Laboratory of Plant Cell Technology, Faculty of Agriculture; Yanagido 1-1, Gifu, Gifu 501-1193, Japan
(E-mail:takita@Cc.gifu-u.ac.jp, Tel:+81-58-293-2911,
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Takita, E., Koyama, H., Shirano, Y., Shibata, D. and Hara, T.
CDNA encoding carrot mitochondrial citrate synthase
Published Only in DataBase (1998) In press
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Daucus carota mRNA for citrate synthase, complete cds.
AB017159
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Pred. No. 0.00e+00;
0; Mismatches 271; Indels 6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 TTAAAGCAGAACATGGAAAGGTTCAGCTGGGAAACATAACTGTTGATATGGTACTTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  512 GIGGAGAACCATIGCCIGAGGGICTGCTCTGCTTTTTAACTGGAAAGGTACCAACTA
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                                                                                                                                                                                  /cell_type="suspension cultured cells"
1. 156
157. 1575
/gene="DcCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"citrate synthase"
/protein_id="BAA32557.1"
/db_xref="PID:d1033521"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 t
                                                                     /organism="Daucus carota"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="PID:g3493367"
/db_xref="GI:3493367"
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1576. .1859
1838. .1843
                                                                                             /cultivar-"MS Yonsun" /db_xref-"taxon:4039"
                                                                                                                                                                                                                                                                                                                                                                                                                      /EC_number="4.1.3.7"
/codon_start=1
Location/Qualifiers
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/gene="DcCS"
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Best Local Similarity 80.7%;
Matches 1155; Conservative
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CMU19481 1733 bp mRNA PLN 04-DEC-1995 Citrus maxima citrate synthase (cit) mRNA, nuclear gene encoding mitochondrial protein, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1232 ACACAGATCCAAGATACATATGTCAGAGAGTTTGCTTTAAAGCATTTACCTGATGATC 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1352 GCAAGGTAAAGAACCCCTGGCCAAATGTTGATGCCCATAGTGGGGGTACTGCTGAATCATT 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1412 ATGGCCTAACAGAAGCCAGATATTATACTGTTCTCTTTGGAGTATCGAGGGCCATTGGTA 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1319 ATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGTGTATCAAGAGCTCTTGGCA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052 CATTAAATGGTTTAGCAGGGCCTCTTCATGGTTTGGCAAATCAGGAAGTTTTGTTATGGA 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1112 TCAAGTCTGTGGTTTCCGAATGCGGAGAAATGTAACTAAGGAACAATTGAAAGATTATA 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1022 TCAAATCTGTTGTAGAGGAGTGTGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTACG 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1142 AGACTGATCCAAGATACACATGCCAGAGAGTTCGCTTTGAAGCATTTGCCTGAAGATC 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1292 CACTCTTTCAATTGGTTTCAAACCTCTTTGAAGTGGTGCCTCCTATTCTTACAGAACTTG 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1202 CACTGTTTCAACTGGTTGCAAAACTCTACGAAGTGTT-CCTCCAATTCTTACAGAACTTG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAAAGTTAA--ACCCTTGGCCAAATGTTGATGCCCACAGTGGTGTTGTTGAACTATT 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1472 TTTGTTCTCAGCTGGTATGGGACAGAGCTCTTGGATTACCACTTGAGAGGCCAAAAAGTG 1531
                                                                                                                                                                                                                                                                                                                                                                                                                      992 CICATACTGGICALCIAGITGCAAGIGCCCTIICAGACCCAIAICTITCTITIGCAGCIG 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                            752 AAACAAAGTATIGGGAGCCAACAIAIGAGGACTCTATIACTITAATIGCTCAATIACCAG 811
                                                                                                     872 ATTCTCTAGATTATGGTGCAAACTTTGCCCACATGCTTGGTTACGATAGTCCCAGCATGC 931
692 GIGICAIGGCCCTCCAGGIICAAAGIGAAIIICAGAAGGCAIACGAGAAAGGGAIICACA 751
                                                                                                                                                                 812 TIGTAGCAGCTTATATCTATCGCAGGATGTACAAGAATGGACAAAGTATATCCACGGATG 871
                                                                                                                                                                                                                                                                                                                                     932 AAGAGCITATGAGGCTTTACGTTACTATCCATACTGACCATGAAGGTGGAAACGTTAGTG 991
                                                                                                                                                                                                                                                                                                                                                                               842 ATGAGCTTATGAAGCTCTATGTCACGATACACAGAGTGATCATGAAGGTGGTAACGTCAGTG 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           citrus maxima
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1532 TTACAATGGAATGGCTTGAAAACCACTGCAAGAAATCTTCTTAAGTTTGAAA 1583
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/db_xref-"d1:624676"
/translation-"AASLRSATALSRLRSRAGOOSNLSNSVRWLOMOSSADLDLHSOL
/translation-"AASLRSATALSRLRSRAGOOSNLSNSVRWLOMOSSADLDLHSOL
REMPIEDQERENKVKSDLGKAQLGNTTIOVVTGGRRGWTGLLWETSLLDAFBADFBGTRFRG
LSTPRCQKLLPAARPOFEPLEGELLWLLLTGRVPSKEQVDGLSKERBRRATVPDYVYK
AIDALPVSAHPWTQFASGVWALQVQSEFQEAVEKGIHKSKSWEPTSEDSLNLTARVPY
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SAHYGHLVAAALSDFYLSFLAALNGLAGPLHGLANDEVLLWIKSVVDECGENVTTEQL
KDYWWTLNSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPDDPLFQLVSKLYEVVPP
ILTKLGKVRNRWPWDVARSOYLLNHFGLAEARYYTVLFGVSRSLGIGSQLIWDRALGL
PLERPKSVTLDWIEKNCKKAA"
                                                                      of acid accumulation in
                                                                                                                    Thesis (1994) Botany & Plant Sciences, University of California at
                                                                                                                                                                                                                                         Submitted (04-JAN-1995) Camilo Canel, University of California at Riverside, Botany & Plant Sciences, Riverside, CA 92521-0124, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    /strain="siamese sweet (purmelo 2240)"
/note="There is a single copy of the cit gene in the citrus genome. A single transcript with an estimated central groups of 1,850 nucleotides can be detected in juice cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111. .1469
/gene="oit"
/function="synthesis of citrate from oxaloacetate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="synthesis of citrate from oxaloacetate and acetylCoA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 GAACCATGGCGTCCCTCAGGAGCGCCACTGCGCTCTTCGCCTTCCGCTTTCGCGTGGGC 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AACAGICTAATCTCAGTAATTCAGTGAGATGGCTTCAAATGCAAAGCTCTGCTGATCTTG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 GAGCCATGGTGTTCTATCGCGGCGTTTCTCTGCTGTCAAAGCTSCGTTCTCGAGCGGTCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Magnoliopsida; Rutanae; Sapindales; Rutaceae; Citrus
1 (bases 1 to 1733)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="citrate synthase precursor"
/protein_id="AAA82743.1"
/db_xref="PID:9624676"
                                            Canel, C., Bailey-Serres, J. and Roose, M. Physiological and molecular genetic studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="juice tissue"
/dev_stage="immature"
1. .56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="citrate synthase"
                                                                                                                                                                                                                                                                                                                                            /organism="Citrus maxima"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:37334"
/sex="hermaphrodite"
/cell_type="juice cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 g
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/gene="cit"
57. .1472
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GIHKSKFWEPTYEDCLIAQVPVVARYYRRWYKNGQVIPLDDSLDYGGNEAHMLGF
DSPQMLELMRLYYTHSDHEGGNYSAHTGHLVGSPELSDPYLGSPAALNGLAGFHGLA
NQEVLLMIKSYVDEGGENISTEQLKDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCORE
FALKHLEDDPFPQLYSKLYEVVPPILLELGKYKNPWPNVDAHSGVLLNHYGLTEARYY
TYLFGYSRSLGIGGLIWDRALGELPERFKSVTMEWLEKFCKRRA"

268 c 370 g 458 L
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
1 (bases 1 to 1551)
1312 GTITIGGCIGAGGCAAGATATTATACTGTTCTTTTTGGAGTATCAAGGAGTCTTGGGATCT 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mueller-Roeber, B., Landschuetze, V. and La, C.U. PROCESSES FOR INHIBITING AND FOR INDUCING FLOWER FORMATION
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Pred. No. 2.29e-268;
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HOECHST SCHENIG AGREVO GMBH (DE)
Other publication DE 4438821 966425
Other publication DE 4435366 960328
Other publication AU 206795 956925
Other publication DE 4408629 956914.
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/strain="2UCHTLINIE 5S 0026"
/db_xref="taxon:3555"
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/db_xref="PID:e306423"
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/clone="PSBCS"
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268 c 370 g 458 t
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La Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B. Plant Cell Physiol. In press
2 (Asses 1 to 1551)
La Cognata,U., Landschuetze,V., Garata,U., La Cognata,U., La Cognata,U., La Cognata,U., La Cognata,U., La Cognata,U.
                        1201 AGTCTTGGAATATGCTCACAGCTTATATGGGACCGAGCTCTTGGCTTGCCGCTAGAGAGG 1260
                                                                                                                                       1369 GCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGCTCTTGGATTGCCACTAGAGGGG 1428
61 CTGAAGAAGATAAAGAAATTTGGAAGTTTCCAGCTGGGGAATATCAATGTTGACATG 120
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Pred. No. 2.29e-268;
0; Mismatches 277; Indels 3; Gaps
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Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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B.vulgaris mRNA for citrate synthase.
X84228
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                                                                                                    181 GAAGAGGTATCCGGTTCAGGGGTTTTTCTATACCTGAATGCCAGAAACTTTTACCCGCT 240
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                         292 GTTCTTGGTGGAATGAGAATGACAGGATTACTGTGGGAAACCTCATTACTTGACCCC 351
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QLKEYVWKTLNSGKVIPGYGHGVLRNTDPRYVCQREFALKHHPDDPLFQCCKLMKLAS
CLTELESEEDWPNVDAHSGVLLNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLA
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LQELIPEHKDRLKKLKSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALG
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YNAIDALPSTAHPMTQFASGVMALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARV
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                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes: Spermatophyta; Magnollophyta; eudicotyledons; Sosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1880)

Unger, E.A., Hand, J.M., Cashmore, A.R. and Vasconcelos, A.C.
Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana
Plant Mol. Biol. 13 (4), 411-418 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 37.5%; Score 655; DB 27; Length 1680; Similarity 76.9%; Pred. No. 7.23e-240; Conservative 0; Mismatches 300; Indels 17; Gaps 16;
                       1369 GCTCTTGGCATTTGCTCTCAGCTAATTTGGGACCGAGCTCTTGGATTGCCACTAGAGAGG 1428
                                                                                                                                                                                                                                             Arabidopsis thallana mRNA for mitochondrial citrate synthetase X17528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TCTTGATCTGCGTTCTGAGCTGCAAGAATTGATTCCAGAACAACAGGATCGCCTAAAGAA 239
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1261 CCAAAGAGTGTCACTATGGAATGGCTTGAAAAGTTTTGTAA 1301
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/db_xref="taxon:3702"
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/product="citrate synthetase"
/protein_id="CAA35570.1"
/db_xref="PID:e1188578"
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/db_xref="GI:2652924"
/db_xref="SWISS-PROT:P20115"
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1301 ACCACTATGGTCTAACCGAAGCAAGGTACTACACCGTGCTCTTTGGTGTTTCAAGGAGTC 1360
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                                                                                                                                                                                  475 CCAICA-AAAGAGCAAGIGGAIICAIIGICICCAGGAAIIGCGAAGICGIGCIACIGICCC 533
                                                                                                                                                                                                                                                                         534 CGATCATGTATACAAAACTATTGATGCCTTACCAGTCACAGCTCATCCAATGACTCAGTT 593
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                                             410 AGTCTGGAGGCTTGAACCATTACCGGAGGTCTTTTGTGGCCTTCTTAACTGGAAAGGTA 469
                                                                                                                                       470 CCTTAGCAAAGAGCAAGTTGAAGCACTGTCGAAAGACTTG-GAAC-CGTGCTGCTGTGTC 527
360 AATTCGCTTTCGGGGCTTGTCTA-TGAATGCCA-AAAGG--TATTACCTGCAGCAA 415
                                                                                           416 AGCCTGGGGGAGAGC-CCTTGCCTGAAGGTCTTCTCTGGCTTCTTTTAACAGGAAAGGTG 474
                                                                                                                                                                                                                                                                                                                                                 528 AGATTATGTGTACAATGCCATCGATGCTCTGCCTTCCACAGGTCATCCAATGACTCAATT
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/translation="MPTKEQYGALSKELRDRALVHDYVFKAIDALPVTAHPWTQFATG
VWALQYQSEFQKAYERGIHKSKYWEPTYEDSLSLIARVPIYASYIYRRIYKDGKVIPW
NDSLYTGGNFSHALGFDSPEWQELMTKYTVHNBISHBEGGNYSAHTGHLVASALSDPYLS
FAAALNGLAGPLHGLANQEVLLWIKSVYEDGGENITTEQLKDYWYKTLNSGKYVPGFG
HGVLRWYPRYTGCREFALKHLPDDPLPQLYGKLYEVYPPYLTQLGGKVKNPWPNVDAH
SGYLLNYYGLTEARXYTVLFGVSRSIGICSQLIWDRALGLPERPKSVTMELLENHCK
                                                                                                                                                                                                                                                                                          1 (bases 1 to 1378)
La Cognata,U., Landschuetze,V., Willmitzer,L. and Mueller-Roeber,B.
Plant Cell Physiol. In press
2 (bases 1 to 1378)
La Cognata,U.
                                                                                                                                    citi gene; cirrate synthase.

Populus balsamifera subsp. trichocarpa X Populus deltoides.

Populus balsamifera subsp. trichocarpa X Populus deltoides

Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

Rosidae; Violales; Salicaceae; Populus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      530 TCCCCGATCATGTATACAAAACTATTGATGCCTTACCAGTCACAGCTCATCCAATGACTC 589
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                     28-OCT-1996
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Submitted (23-JAN-1995) U. La Cognata, Institute fuer
Genbiologische Forschung, Berlin GmbH, Ihnestrasse 63, 14195
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Pred. No. 3.18e-216;
0; Mismatches 196; Indels 3;
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/transl_except=(pos:16. .18,aa:Met)
/product="citrate (si)-synthase"
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               PHCITSYNH 1378 bp mRNA P
Populus hybrid mRNA for citrate synthase.
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254 CTCGTGTGCCAATAGTAGCTTCATATTTATCGAAGGATTTACAAAGATGGGAAAGTTA 313

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Direct Submission Submission Submilted (06-FBE-1998) Molecular Cardiology Institute, 75 Raritan Avenue, Highland Park, NJ 08904, USA Location/Qualifiers
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                                                                     314 TTCCTATGAATGACTCTTTGGTTATAGGTGGAAATTTTTCACACATGTTGGGATTTGATA 373
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning and sequence analysis of human citrate synthase cDNA
374 GICCIGAAAIGCAAGAGCITAIGAGGCITTAIGTIACTAACCAIAGIGACCAIGAAGGIG
                                                                                                                                                                                  770 TACCTAAGGATGACTCACTGGATTATGGTGCAAATTTTGCTCACATGCTTGGTTCAGTA
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                                                                                                                                                                                                                                              434 GGAATGTCAGTGCTCATACTGGTCACCTGGTTGCTAGTGCACTTTCAGATCCTTATCTTT
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Homo sapiens citrate synthase mRNA, complete cds.
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Goldenthal, M.J.
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2 (bases 1 to 1401)
Goldenthal, M.J.
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NLYWEGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELMRLYLTIHSDHEGGNVSAHTSH
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TANSGRVPGOYGHAVLRKTDPRYTQQREFALKHLPNDPMFKLVAQLYK IVPNVLLEQG
TAKNDWDNVDAHSQYLLQYYGMTEMNYTTVLEGVSRALGVLAQLIWSRALGFPLERPK
SMSTEGLMKFVDSKSG"
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QARIKTFRQQHGKTVVGQITVDMMYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPECQ
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Pred. No. 2.34e-88;
0; Mismatches 458; Indels
                                                                                                                                       /note-"isolated from a 22-year old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 t
                                                                                                                                                                                                                     /product="citrate synthase"
/protein_id="AAC25560.1"
/db_xref="PID:93288815"
                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                     /tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 g
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                                                                                                                                                                                              /codon_start=1
                                                                             /sex="male"
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Local Similarity 62.3%;
hes 768; Conservative
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RARKTKTROGGGNTVVGQITYDMMYGGMRGBKGLYETSVLDPDEGIRERGYSIPECO

RALFAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRALFSHVVTMLDNFT

NLHPMSQLSAAITALNSESNFARAYAEGIHFKTKYWELIYEDCMDLIAKLPCVAAKIYR

NLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSH
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Vertebrata; Eutheria; Artiodactyla; Suiformes; Sıina; Suidae; Sus.
1 (bases 1 to 1455)
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                                                                                                                                                                                                                                                                                                      1165
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                                                                                                                                                                                                                                                                                                                                         1226 TCTACGA-AGTGTTCCTCCAATTCTTACAGAACTTGGCAAAGTTAA--ACCCTTGGCCAA 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1283 ATGTTGATGCCCACAGTGGTGTTGTTGAACTATTATGGTTTAACTGAAGCAAGATATT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1343 ATACGGTCCTCTTTGGTGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGGGACC 1402
                                                                                                                                                          986 TTCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTG 1045
                                                                                                                                                                                              959 GCAAAGATGTGTCAGATGAGAAGTTACGAGACTACATCTGGAACACACTCAACTCAGGAC 1018
                                                                                                                                                                                                                              1046 GGGAGAACATTTCCAAAGAGCAGTTGAAAGACTACGCTTGGAAAACATTGAAAAGTGGCA 1105
                                                                                                                                                                                                                                                                                                                                                                                                             1139 IGTACAAGATIGIGCCCAAIGICCICTIAGAGCAGGGIAAAGCCAAGAAICCITGGCCCA 1198
                                                                                      926 GTGCTTTGTCAGACCCTTACCTCTCCTTCGCTGCTTTGAATGGTTTAGCTGGACCAC 985
                                                                                                                        839 GIGCCCTITCCGACCCTTACCTGICCTTTGCAGCAGCCATGAACGGGCTGGCAGGGCCTC 898
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                                                                                                                                                                                                                                                                                                                                                            Evans, C.T., Owens, D.D., Sumegi, B., Kispal, G. and Srere, P.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="citrate synthase precursor (EC 4.1.3.7)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M21197.1 GI:164418
citrate synthase.
Porcine kidney, cDNA to mRNA, clone PCS4.
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/protein_id="AAA31017.1"
/db_xref="PID:9164419"
/db_xref="GI:164419"
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Biochemistry 27, 4680-4686 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               749 IGTACAAGAACGGCAACACTATACCTAAGGAIGACTCACTGGAITA-IGGIGC-A-AATI 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           725 TCACCAACATGTTAGGCTATACTGATGCTCAGTTCACGGAGCTCATGCGCTTGTACCTCA 784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 IGGGCCAAATCACTGTGGACATGATGTATGGTGGCATGAGAGGCATGAAGGGATTGGTGT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 TGGGAAACATCACAGTTGATATGGTTCTTGGTGGAATGAGAGGAATGACAGGATTACTGT 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 AATGCCAAAAGGTATTACCTGCAGCAAAGCCTGGGGGAGAGCCCTTGCCTGAAGGTCTTC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 422; Indels
                                                                                                                                       8. .88
/note="citrate synthase signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 273; DB 23;
Pred. No. 5.77e-88;
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/clone="Plasmid pFCS1 (Suissa et al., EMBO J. 3, 1773-1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                        1204 AATGTGGATGCTCACAGTGGGGTGCTGCTCCAGTACTATGGCATGACGGAGATGAACTAC 1263
                                                                                                                                                                                                                                                        1264 TACACAGTCCTGTTCGGGGTATCACGGGCACTGGGTGTATTAGCACAGCTCATCTGGAGC 1323
1084 CAAAGAGAGTITGCTCTGAAACACCTGCCTCATGACCCCCATGTTTAAGCTGGTTGCTCAG 1143
                                                                                                                           1225 CICTACGAAGTGTICCICCAATICITACAG-AACTIGGCAAAGTIAA--ACCCIIGGCCA 1281
                                                                                                                                                                                                              1282 AATGTTGATGCCCACAGTGGTGTTGTTGAACTATTATGGTTTAACTGAAGCAAGATAT 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (05-JUL-1993) Peter Lindner, Protein Engineering,
Max-Planck-Institut fuer, Biochemie, Am Klopferspitz 18a,
Martinsried, D-82152, Fed. Rep., Germany
4 (bases 1 to 14R1)
Suissa,M., Suda,K. and Schatz,G.
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening method
EMBO J. 3 (8), 1773-1781 (1984)
                                                                                                                                                                                                                                                                               SCMTCISNA 1481 bp DNA PLN 17-FEB-1997
S.cerevisiae mitochondrial citrate synthase gene, complete CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"SGD:L0000341"

/db_xref-"SGD:L0000341"

/product-xperimental
/product-"the processing site has been determined by direct N-terminal protein sequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1481)
Lindner,P and Plueckthun,A
The effect of point mutations in the hinge of yeast citrate
                                                                                       1144 CIGTACAAGATTGIGCCCAATGTCCTCCTGGAACAGGCCAAGGCTAAGAATCCTTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thesis (1993) Protein Engineering, Max-Planck-Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Saccharomyces cerevisiae"
/strain="D273-10B"
/db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                           1324 CGAGCCTTAGGCTTCCCTCTAGAGGGCCCAAG 1356
                                                                                                                                                                                                                                                                                                                                                                                    1402 CGAGCTCTTGGATTGCCACTAGAGGGCCAAAG 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"SGD:L0000341"
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baker's yeast.
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EHVIOLLDSLPRÜLHPMAGFSIAVTALESESKFAKAYAGGVSKKEYWSYTFEDSLÜL
GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAGLLGYENKDFIDLMKLYLTIHSDH
EGGNYSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANDEVLEWEFKLREEVKGDY
SKGINSTAHTTHLVGSALSSPYLSLAGLNGFARDPRYTAGREFALKHFPDYELFKLYSTIY
EVARCVLIKHGKTKMPNNDSHSGYLLOYYGLTEASFYTVLFGVARAIGVLPOLIID
RAVGAPIERPKSFSTEKYKELVKKIESKN"
                                                                                                                                                                                                  LKERFABIIPAKABEIKKFKKEHGKTVIGEVLLEQAYGGMRGIKCLVWEGSVLDPEEG
IRFRGRTIPEIQRELPKABGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARSEIP
                                                                                                                                                                          /translation-"MSAILSTISKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 GGGTAGTACAGAACCTTTGCCAGAAGCTTTATTTTGGTTGCTTTTGACTGGTGAAATACC 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 TGGTGGTATGAGAGGTATTAAAGGCCTTGTTTGGGAAGGTTCCGTGTTAGACCCCGAAGA 302
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                /db_xref="SGD:L0000341"
/product="mitochondrial citrate synthase"
/protein_id="CAA8078:1"
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/codon_start=1
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Best Local Similarity 60.3%;
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baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomyceta; Hemiascomycetes; Saccharomycetales;
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1 (Dases 1 to 2427)
Suissa,M., Suda,K. and Schatz,G.
Isolation of the nuclear yeast genes for citrate synthase and fifteen other mitochondrial proteins by a new screening method EMBO J. 3 (8), 1773-1781 (1984)
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                                                                                                                                                                                                                                    1076 ACTACGCTIGGAAAACATIGAAAGIGGCAAGGITGTCCCIGGTITCGGACAIGGAGTIC
                    843 ITCTGCCCATACTACACATTTAGTGGGTTCTGCCTTATCTTCGCCATACTTATCTTTGGC
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 783 ITITAITGACTIAAIGAGACTATAITIAACIAITCAITCIGATCAIGAAGGIGGIAACGI
                                                                                                                                                                                                              963 AIGGCIATITAAAITGAGAGAAGAAGIGAAAGGIGACIATICAAAAGAAACAAITGAAA-
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/protein_id="CAA25359.1"
/db_xref="PID:93603"
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Yeast gene for citrate synthase.
X00782
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CALEVLASKTYRNVEKDGKTISTDPARDSCKRUADGLGGFBUKDFIDLMRLYLTIHSD
HEGGNVSAHTTHLVGSRLSSPYLSLAMGLNGLAGPLHGFRANGEVLEMLFKLREEVKGD
YSKETIEKYLMDTLNAGRVVPGYGHAVLRKIDPRYTAQREFALKHFPDYSELFKLVSTI
YSKAPGVLTKHGKTKNPWPNVDSHSGYLLQYYGLTEASFYTVLFGVARAIGVLFOLII
DEAVAAPIERPKSFSTEKYKELVKKIESKN"
4 439 C 414 49 T 757 L
                      /translation="MSAILSTTSKSFISRGSTRQCQNMQKALFALLNARHYSSASEOT
LKERFAEIIPAKAQEIKKFKKEHGKTVIGEVLLEEQAYGGMRGIKGLVWEGSVLDPEE
GIRFRGRIIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARSEI
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                                                                                                                                                                                                                                                                                                                                                          Score 210; DB 27; Length 2427; Pred. No. 1.94e-63;
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/db_xref="SWISS-PROT:P00890"
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Best Local Similarity 60.3%;
Matches 688; Conservative
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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1460 TGAGAAAACTGATCCTCGTTATACGGCTCAACGTGAATTCGCATTGAAACATTTCCCAG 1519
                                          1136 TGCGCAAGACTGATCCAAGATACACATGCCAGAGAGAGTTCGCTTTGAAGCATTTGCCTG 1195
                                                                                       1520 ATTACGAGTTATTTAAGTTGGTCTCCACCATTTATGAAGTTGCCCCAGGGGTTTTAACTA 1579
                                                                                                                                                                        1580 AGCATGGTAAAACTAAGAACCCATGGCCAAATGTTGATTCACATTCCGGTGTTTTATTGC 1639
                                                                                                                                                                                                                 1255 AACTTGGCAAAGTTAA--ACCCTTGGCCAAATGTTGATGCCCACAGTGGTGTTGTTGTTGA 1312
                                                                                                                                                                                                                                                            1640 AATACTATGGTCTAACTGAGGCTTCGTTCTACACTGTATTGTTTGGTGTTGCCACAGGCTA 1699
                                                                                                                                                                                                                                                                                  1700 TIGGIGIGITACCCCAATTAATCATCGATAGGGCTGTTGGTGCTCCAATCGAAAGGCCAA 1759
                                                                                                                                                                                                                                                                                                                                                                        1373 TIGGCATITGCTCTCAGCTAAITIGGACCGAGCTCTGGATIGCCACTAGAGAGGCCAA 1432
                                                                                                                              1196 AAGATCCACTGTTTCAACTGGTTGCAAAACTCTACGAAGT-GTTCCTCCAATTCTTACAG 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCYNROO1C 4391 bp DNA PLN 11-P
S.cerevisiae chromosome XIV reading frame ORF YNROO1C.
271616 <u>Y13139</u>
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Aert.R., Verhasselt,P., Voet,M. and Volckaert,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"PID:91302469"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="CEN element CDE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="CEN element CDE II"
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/note="CEN element CDE I"
150. 234
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/gene="CIT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"SGD:L0000341"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome-"XIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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EHVIQLLDSLPRÜLHPMAQFSIAVTALESESKFAKAYAQGVSREYWSYTFEDSLDLL
GKLEVIASKIYRNYFKDGKITSTDPNADYGKNLAQLLGYERNDFIDLMRLYLTIHSDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1064 ITTGGCCTTTCGATTGGAGCACCAACAGCCCTATCGATGATTAATTGGGGTAACACACCA 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCAATAAAACACCGGAATGTGAATCAACATTTGGCCATGGGTTCTTAGTTTTACCATGC 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1424 T-TTTCAATTGTTTCTTTTGAATAGTCACCTTTCACTTCTTCTTCTCAATTTAAATAGCCA 1482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1433 TITGGCCTCTCTAGTGGCAATCCAAGAGGTCGGTCCCAAATTAGCTGAGAGCAAATGCCA 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1124 ATAGCTCTGGCAACACCAAACAATACAGTGTAGAACGAAGCCTCAGTTAGACCATAGTAT 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1313 TTCAACAACACACCACTGTGGGCATCAACATTTGGCCAAGGGTT--TAACTTTGCCAAGT 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1244 TTAGTTAAAACCCCTGGGGCAACTTCATAAATGGTGGAGACCAACTTAAATAACTCGTAA 1303
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complement(31230. 3301)
/opene="tryf kGG, NR" - systematic name"
/note="anticodon gene: AGG; tRNA-Pro2 - common name"
/opene="tryf kGG, NR" - systematic name"
/gene="tryf kGG, NR" - systematic name"
complement(3380. 3497)
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/gene="tN(GTT)NR - systematic name"
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3983. .4056
/gene="tN(GTT)NR - systematic name"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1304 TCTGGGAAATGTTTCAATGCGAATTCACGTTGAGCCGTATAACGAGGATCAGTTTTTCTC
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/note="solo-tau"
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1783 TAATTTACCCAGCAGATCTAACGAATCTTCAAATGTATAGCTCCAATATTCTTTGTTGGA 1842
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                                                                                                                                                                        1903 AGAAAATIGCGCCATIGGATGTAGATCTTTIGGGAGGCTATCTAAAAGTIGGATAACGTG 1962
                                                                                                                                                                                                                                1963 CTCTGGAATTTCTGATCTGGCAGCTAAATCAGCAGAAAGGGCTTTAACTTGAGCGTCAGT 2022
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                                                                                                                                                                                                                                                                                                                                                                                                     2143 ITCTICGGGGTCTAACACGGAACCTICCCAAACAAGGCCTTTAATACCTCTCATACCACC 2202
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- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch\_nn MasPar time 392.61 Seconds 953.450 Million cell updates/sec Sat Oct 23 22:01:39 1999; Run on:

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1 GCTCTTGGGATCTATTTCT.......aaaaaaaaaaaaaaaaa 1747 CGAGAACCCTAGAIAAAGGA......ITTTTTTTTTTTTTTTTT

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Dbase 0; Query 0

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SID

Nmatch

271905 seqs, 107135622 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq35
l:part1 2:part2 3:part3 4:part4 5;part5 6:part6 7:part7 8:part8 12:part1 2:part12 13:part13 8:part8 14:part14 15:part15 112:part12 13:part13 14:part14 15:part15 16:part16 17:part27 18:part18 20:part20 21:part22 23:part22 23:part23 24:part24 25:part25 25:part26 27:part23 23:part23 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 40:part46 47:part44 45:part45 46:part46 47:part44 45:part45 46:part46 47:part46 47:part48 49:part49 50:part50 51:part51 52:part52 53:part53 54:part54 55:part55 56:part56 57:part57 58:part58

Mean 9.616; Variance 7.859; scale 1.224 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description Pred. No.	Tobacco citrate synth 0.00e+00				Base substituted E.co 7.45e-08		Base substituted E.co 1.44e-06		
OI.	T04201	T04199	T03410	T04200	N81164	T31478	N81164	T28255	0000
DB									
% Query Match Length DB	1747	1891	1891	1551	204	3437	204 1	1558	
% Query Match	100.0	70.9	70.9	41.6	5.6	5.6	2.5	2.5	(
Score	1747	1238	1238	726	46	46	43	43	
Result		7	e	4	Ŋ	ø	7	œ	(

100.0%; Score 1747; DB 16; Length 1747;

Query Match

.44e-0 .44e-0 .39e-0 .64e-0 .64e-0	. 046 . 016 . 016 . 646 . 646 . 786 . 786	.89e-0 .89e-0 .89e-0 .78e-0 .78e-0	6.89e-05 6.89e-05 1.78e-04 1.78e-04 1.78e-04 1.78e-04 6.89e-05 6.89e-05
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## ALIGNMENTS

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DNA encoding plant citrate synthase - used to regulate flower formation,
                                                                                                                                                                                                                                                                                                                                           to improve storage of tubers, etc. and to reduce sprouting claim 7; Page 60-63; 87pp; English. To identify a CDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepured plaques of this cDNA bank were screened using a radioactive DNA probe which comprises Solanum tuberosum citrate synthase cDNA probe which comprises Solanum tuberosum citrate synthase cDNA (104199). One of the clones was sequenced. The nt. sequence is given in T04201.
                                                                                                                                                                                                                                         (AGRE ) HOECHST-SCHERING AGREVO GMBH.
La Cognata U, Landschutze V, Muller-rober B, Landschuetze Muellar-rober B,
P-PSDB; R82840.
                             25-JAN-1996 (first entry)
Tobacco citrate synthase cDNA.
Citrate synthase; flower formation; ss.
Nicotiana tabacum
T04201 standard; cDNA to mRNA; 1747
                                                                                               Location/Qualifiers
70..1476
/*tag= a
                                                                                                                                                              14-SEP-1995.
07-MAR-1994; DE-40859.
09-MAR-1994; DE-408629.
22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
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DNA encoding plant citrate synthase - used to regulate flower formation,
1021 ATCAAATCTGTTGTAGAGGAGTGTGGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTAC 1080
                                                                    gcttggaaaacattgaaaagtggcaaggttgtccctggtttcggacatggagttctgcgc 1140
                                                                                                                                  1081 GCTTGGAAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGC 1140
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Potato citrate synthase cDNA.
Citrate synthase; flower formation; tuber storage; ss.
Solanum tuberosum.
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La Cognata U, Landschutze V, Muller-rober B,
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09-MAR-1995; E00859.
09-MAR-1994; DE-408629.
22-SEP-1994; DE-43366.
19-OCT-1994; DE-438821.
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P-PSDB; R82838.
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to improve storage of tubers, etc. and to reduce sprouting claim 5; Page 53-56; B7pp; English.

To identify a cDNA from potato which codes for citrate synthase, a cDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of introduce BamHI clavage sites at both ends of the amplified cDNA firsyment, a cDNA library was prepd. from potato leaves and screened with A. thaliana clirate synthase cDNA, Positive clones were purified and sequenced. Then ts sequence is given in T04199. Sequence 1891 BP; 512 A; 370 C; 425 G; 584 T;
                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 93; Indels 18; Gaps
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Local Similarity 92.8%;
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876 aatacacagtgatcatgaaggtggtaatgtcagtgctcacacccggtcacttggttgctag 935
                                    1047 GGAGAACATTTCCAAAGAGCAGTTGAAAGACTACGCTTGGAAAACATTGAAAAGTGGCAA
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Citrate synthase; inhibitor; increased storage capacity; potato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Landschutze V, Muller-Roeber B, Landschuetze V;
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09.MAR-1994; 408629.

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19.OCT-1994; DE-438821.
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P-PSDB; R86383.
Inhibiting citrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 GGTAAAAGTTAATTTGTT-GATTTTTGCGAGCCATGGTGTTCTATCGCGGCGTTTCTCTG 96
also new CS sense and anti-sense DNA sequences
Claim 6; Page 15-19; 35pp; German.
The potato citrate synthase (CS) gene or CDNA sequences. CS DNA
sequences are useful for altering CS activity in plants. Antisense
CS sequences are useful for altering CS activity in plants. Antisense
CS sequences can be used to inhibit CS expression in plants and has
the effect of inhibiting flower formation and by doing so improves
the plant's storage capacity. This is partito. useful in corp plants
of any kind but esp. useful in potatoes. In addition to altering CS
activity the DNA sequences can also be used to identify similar
sequences in the genomes of other plants and in the production of
transgenic plants with altered CS activity.
Sequence 1891 BP: 512 A; 370 C; 425 G; 584 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgcagagtcgggcatcatatccctgatcatcatgtatacaactattgatgccttaccagt
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0.00e+00;
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Local Similarity 92.8%;
nes 1439; Conservative
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DNA encoding plant citrate synthase - used to requlate flower formation, to improve storage of tubers, etc. and to reduce sprouting
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                                                                                                                                                                                                                                                                                           1047 GGAGAACATTICCAAAGAGCAGTIGAAAGACTACGCTIGGAAAACATIGAAAAGTGGCAA 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1467 CAAGAAAGCAIGATTIGTTIGAAAICTCTGCGAGCATAAAAGCACAAIGTAAAAICTITA 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1476 caagaaagcatgaattgtttgaaatctc-gcgagcataaaa-cacaatgtataatctcta
                                                                                                                                                                                                          987 TCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTTGTAGAGGAGTGTGG
                                                                                                                                                                                                                                                                                                                                     1116 ggttgtccctggttttggacatggagttctgcgaaagactgtaccaagatatacatgcca
                                                                                                                                                                                                                                                                                                                                                                            1107 GGIIGICCCIGGIIICGGACAIGGAGIICIGCGCAAGACIGAICCAAGAIACACAIGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1236 ctacgaagttttcctcctgttcttacagaacttggcaaagttaaaaccttggccaaatgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1296 tgatgcccacagtggtgtgttgttgaactattatggtttaactgaagcaagatattatac
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876 aatacacagtgatcatgaaggtggtaatgtcagtgctcacacccggtcacttggttgctag
                                       867 GATACACAGTGATCATGAAGGTGGTAACGTCAGTGCTCACACAGGTCACTTGGTTGCTAG
                                                                                                                        927 IGCITIGICAGACCCTIACCICTCCTICGCIGCTGCTITGAAIGGITIAGCIGGACCACI
                                                                                                                                                                                                                                                                                                                                                                                                                      1176 gagagagttegetatgaageatttgeetgaagateeaetgttteaaettggttteaaaaet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1227 CTACGAAGTGTTCCTCCAATTCTTACAGAACTTGGCAAAGTTAAAACCTTGGCCAAATGT
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                                                                                     tgetttgtetgateettaceteteetttgetgetgetttgaatggtttageeggaeeaet
                                                                                                                                                                  996 tcatggtttagccaatcaggaagttttgctatggataaaaatctgttgtagaagaatgtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugar beet citrate synthase cDNA.
Citrate synthase; flower formation; ss.
Beta vulgaris strain Zuchtlinie 5S 0026
Key
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19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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07-MAR-1995, E00859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 gaagagggtatccggttcaggggtttttctatacctgaatgccagaaacttttacccgct 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cogotiggatgactocottgattatggtggaaatttogcacacatgttgggatttgatago 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         772 CCTAAGGATGACTCACTGGATTAIGGIGCAAATTTIGCICACATGCITGGTTTCAGTAGC 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 cctcagatgcttgagctgatgcgcctttatgtcacaattcacagtgatcatgagggtgga 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                892 AACGICAGIGCICACACAGGICACTIGGIIGCIAGIGCIIIGICAGACCCIIACCICICC 951
                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ctgaagaagaagaaagaatttggaagtttccagctggggaatatcaatgttgacatg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 GTTCTTGGTGGAATGAGAATGACAGGATTACTGTGGGAAACCTCATTACTTGACCCC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 CCCGAICATGTATACAAAACTATTGATGCCTTACCAGTCACAGCTCATCCAATGACTCAG 591
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                                                                                                                                                                                                                                                                                                                                                                                             172 TCTTCTGGTCTTGATCTGCGTTCTGAGCTGCAAGAATTGATTCCAGAACAACAGGATCGC 231
                                                                                                                                                                                                                                                                                                                                                1 tectetaacettgacettegtteagagttacaagaactgatteetgaacaacaggaacga 60
Claim 6; Page 57-60; 87pp; English.

To identify a cDNA from sugar beet which codes for citrate synthase, a cDNA bank of leaf tissue from sugar beet was prepersorable sport and sugar sugar specifications of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solanum tuberosum citrate synthase cDNA (T04199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 GIGCCATCAAAAGAGCAAGIGGATICATIGICICAGGAATIGCGAAGICGIGCTACIGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 CTAAAGAAGCTCAAGTCAGAGGATGGAAAGGTTCAATTGGGAAACATCACAGTTGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ccagaccatgtgtacaaaacaattgatgctctacctattacggctcatccaatgactcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592 TITIGCTACTGGAGTCATGGCTCTTCAGGTTCAAAGTGAATTTCAAAAGGCATATGAGAAA
                                                                                                                                                                                                                                              Score 726; DB 16; Length 1551;
Pred. No. 0.00e+00;
0; Mismatches 277; Indels 3
                                                                                                                                                                                                      458 T;
                                                                                                                                                                                                      370 G;
                                                                                                                                                                                                                                                 tch al Similarity 78.5%; Pred. No. 0 1021; Conservative 0; Mismat
                                                                                                                                                                                                      268 C;
                                                                                                                                                                                                   455 A;
                                                                                                                                                                                                      1551 BP;
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Introducing random point mutations into nucleic acods introducing random point mutations into nucleic acods in introducing random point mutations of molecules and screening.

This proporation, completion of molecules and screening.

Disclosure: p: English.

Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nuclectide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
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                                          1251 ACAGAACTIGGCAAAGITAA - ACCCTIGGCCAAAIGTIGAIGCCCACAGIGGIGIGIIG 1308
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901 aaagattatgtttggaagacactaaacagtggcaaggttgtacctggatttggtctagga
                                                                                                                                                                gtattgcggaagacagatccaagatacacatgccaaagagaatttgcgttgaagcacttg
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Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6%; Score 46; DB 1; Length 204; 8.7%; Pred. No. 7.45e-08;
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Claim 1, Page 64-67, 90pp; English.

A partial cDNA clone (T31478) codes for a spinach debranching enzyme (DE) (R98371) useful for modifying the branching degree of amylopectin synthesised in plants. It was obtd. by PCR amplification of cDNA from a spinach leaf cDNA library using probes (T31480-81) based on DE peptides (R98385-86). The clone can be incorporated into a vector and used for prodn. of recombinant DE, or used in the breeding of transgenic plants; transgenic potatoes showed increased DE activity properties. Ribozyme or antisense sequences can be used to reduce the DE activity of transgenic plants. The modified starches have clood and industrial applies.

Sequence 3437 BP; 1002 A; 676 C; 727 G; 1032 T;
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Debranching enzyme; R enzyme; spinach; potato; amylopectin; starch;
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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11.9%; Pred. No. 7.45e-08;
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                                                              154 ccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                       | : ::: :: ::: :::: | 811 CACATGCTTGGTTTCAGTAGCTCTGACATGCA 842
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T31478 standard; cDNA to mRNA; 3437 BP.
T31478;
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22-DEC-1995; E05091.
22-DEC-1994; DE-447387.
(GENB-) INST GENBIOLOGISCHE FORSCHUNG.
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201..3095
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N81164 standard; DNA; 204 BP.
N81164;
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nes 59; Conservative
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WPI; 96-309595/31.
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                                                                 Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
Disclosure, p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                      Single stranded template and an oligonucleotide was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred shaquarly in any given mutant.
                                                                                                                                                                       Random point mutations were introduced into the alpha fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 hyvybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1031 ACAGATTTGATCCATAGCAAAACTTCCTGATTGGCTAAACCATGAAGTGGTCCA 978
             Lebtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI: 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Survival motor neuron gene, clone T-BCD541.
Survival motor neuron; SMN: spinal muscular atrophy, SMA;
T-BCD541; C-BCD541; amytrophic lateral sclerosis; ALS;
primary lateral sclerosis; PLS; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 1; L
Pred. No. 1.44e-06;
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/note= "beginning of exon 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "beginning of exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 C;
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/note= "beginning
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T28255 standard; cDNA; 1558 BP.
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Best Local Similarity 13.2%;
Matches 15; Conservative
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(SUSO) SUOMEN SOKERI OY.
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13-0CT-1996
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/label= Exon-8

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EP-711833-A2.
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                                                                                                                                                                                                                                                                                                                                                                         New isolated survival motor neuron gene - used to develop prods. for the diagnosis and treatment of motor neuron diseases Claim 1: Fig 3A: 29pp; English and control of the SMN gene is a chromosome 5-SMA (Spinal Muscular Atrophy) determining gene. Sequences of clone T-BCD541 and clone C-BCD541 are provided in T28259, respectively.

SMN sequences can be used for detecting neuron disorders having symptoms of muscular weakness with or without sensory changes
                                                                                                                                                                                                        Query Match 2.5%; Score 43; DB 22; Length 1558;
Best Local Similarity 84.1%; Pred. No. 1.44e-06;
Matches 53; Conservative 0; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                           02-007-1996 (first entry)

Human survival motor neuron gene cDNA clone T-BCD541.

Survival motor neuron gene; SMN gene; spinal muscular atrophy;
chromosome 5-SMA determining gene; amytrophic lateral sclerosis;
primary lateral sclerosis; arthrogryposis multiplex congenita;
diagnosis; gene therapy; T-BCD541; ss.
                                                                                                                                                                     such as amytrophic lateral sclerosis (ALS), SMA, primary lateral
                                                                                                                                                                                        402 T;
                                                                                                                                                                                        336 G;
                                                                 (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Melki J, Munnich A;
                       /note= "beginning of exon 8"
                                                                                                                                                                                        283 C;
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 34..918
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/label=_Exon-6
868..921
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/label= Exon-7
922..1483
/*tag= i
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T18828 standard; cDNA; 1560 BP.
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/label= Exon-5
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/label= Exon-2
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/label= Exon-3
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/label= Exon-4
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                                       24-APR-1996,
19-OCT-1994; 402353.
19-OCT-1994; EP-402353.
                                                                                                                                                                              sclerosis (PLS), etc.
Sequence 1558 BP;
                                                                                 WPI; 96-202055/21.
                                                                                          P-PSDB; R96991
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Welki J. Munnich A. Munnich A. Melki J. Munnich A. Munn
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                                                                                                                                                                                                                                                                                                                                                                                                                         murine equiv. - useful to develop primers and probes for in vitro detection of motor neuron diseases e.g. spinal muscular atrophy a Claim 1: Fig 3: 47pp; English.
A CDNA sequence (T18828) was detd. for the human survival motor neuron (SMN) gene T-RCD541 (see also T18868). This telomeric gene is responsible for motor neuron diseases of the spinal muscular atrophy (SMA) type. The SMN gene is lacking or truncated in 98% of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atrophy (SWA) type. The SMN gene is lacking or truncated in 98% of SWA patients. The gene was discovered using a complex system of restriction mapping, distinguishing the Erel from the Eren by Southern blot, and determination of the differences between the Erel in SWA patients by genetic and physical mapping. It can be used in gene therapy protocols to correct disorders present in SWA, anytrophic lateral sclerosis, primary lateral sclerosis and arthrogryposis multiplex congenita patients, to produce large quantities of recombinant SMN protein (see also R94963), and to design probes and primers (118833-65) useful for detecting or
                                                                                                                                                                                                                                                                                                                                                                                       Human survival motor neuron gene T-BCD541, variant C-BCD541 and
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Survival motor neuron; SMN; spinal muscular atrophy, SMA;
T-BCD541; C-BCD541; amytrophic lateral sclerosis; ALS;
primary lateral sclerosis; PLS; ss.
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19-0CT-1994: 402353.
19-0CT-1994: EP-402353.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                              (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. Melki J, Munnich A;
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T28259 standard; cDNA; 1582 BP.
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13-OCT-1996 (first entry)
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15-MAY-1996.
19-OCT-1995; 402335.
19-OCT-1994; EP-402353.
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Sequence 1560 BP;
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P-PSDB; R94963.
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                                                                                                                                                                                                              Human survival motor meuron variant gene cDNA clone C-BCD541.
Survival motor neuron gene: SNN gene: spinal muscular atrophy:
chromosome 5-SNA determining gene: amytrophic lateral sclerosis;
primary lateral sclerosis; arthrogryposis multiplex congenita;
diagnosis; gene therapy; C-BCD541; ss.
 Score 43; DB 22; Length 1582; Pred. No. 1.44e-06;
                          0; Mismatches 10; Indels
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/note= "base 873 (t) is c is T-BCD541"
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19-0CT-1995; 402335.
19-0CT-1994; EP-402353.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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/label= Exon-2
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/label= Exon-6
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/label= Exon-4
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Query Match 2.5%;
Best Local Similarity 84.1%;
Matches 53; Conservative
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WPI; 96-232098/24
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Human secreted protein; quel 178 clone HETAR54.

Human; secreted protein; quel protein; quel therapy; protein therapy;

Human; secreted protein; fusion protein; quel therapy; protein therapy;

Human; secreted protein; lumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal; developmental abnormality; foetal deficiency; blood; allergy; renal; dinflammation; ischaemic shock; Alzheimer's disease; restenosis; Imphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schlorbenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtlis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                          Ouery Match 2.5%; Score 43; DB 22; Length 1582;
Best Local Similarity 84.1%; Pred. No. 1.44e-06;
Matches 53; Conservative 0; Mismatches 10; Indels 0; Gaps
of sequence within intron 7 of the C-BCD541 genomic sequence results in an alternatively spliced transcript that lacks exon 7 and a truncated SMN protein (R94965) lacking the exon 7-encoded C-terminal region. 562 A; 283 C; 335 G; 402 T;
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US-048884.
US-048893.
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US-048962.
US-048970.
US-048974.
US-049373.
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18-DEC-1997; US-070923
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WO9854963-A2.
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06-JUN-1997;
06-JUN-1997;
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345 C;

575 A;

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Seguence 1848 BP;
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Claim 4; Page 440-441; 772pp; English.
The invention relates to nucleic acid sequences (V84411 to V84633)
encoding human secreted proteins (W88534 to W88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 209019, 209080, 209081, 209082, 209077, 209078, 209088, 209089, 209010, 209081, 209081, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 209083, 
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New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological
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Brower LA, Carter KC. Dillon PJ, Ebner R, Endress GA, Fan P. Fend P. Ferrie AM, Fischer CL, Florence C, Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z; WPI; 99-053665/05.
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US-048898.
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US-057646.
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05-SEP-1997; US-057666.
05-SEP-1997; US-057760.
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US-048876.
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US-048963.
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05-SEP-1997; US-057769.
05-SEP-1997; US-057774.
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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05-SEP-1997;
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Human secreted protein gene 120 clone HHPTD20.
Human secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue, cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflaumation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane protein(s) BA0306 and BA2303 - useful for, e.g. treatment and prevention of arteriosclerosis and restenosis Claim 16; Page 90-95; 141pp; Japanese.
This sequence encodes the human BA0306 membrane protein of the invention.
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                                                                                                                                                                                                                                                                                        17-DEC-1998 (first entry)
Human membrane protein BA0306 coding sequence.
Membrane protein; BA0306; BA2303; arteriosclerosis; coronary restenosis;
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Sequence 2519 BP; 766 A; 439 C; 809 T;
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                                                     Gaps
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Ouery Match 2.5%; Score 43; DB 56; Length 1848; Best Local Similarity 97.8%; Pred. No. 1.44e-06; Matches 44; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_except= (pos: 1015...1017, aa: Xaa)
/transl_except= (pos: 1492...1494, aa: Xaa)
/transl_except= (pos: 1582...1584, aa: Xaa)
/transl_except= (pos: 1582...1584, aa: Xaa)
/transl_except= (pos: 1609...161, aa: Xaa)
/transl_except= (pos: 1693...1695, aa: Xaa)
/transl_except= (pos: 1693...1695, aa: Xaa)
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                                                                                                     /transl_except= (pos: 1693..1695, aa:/note= "Xaa= unspecified amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 1..1785
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Nakamura Y, Tanaka T, Tsukada S;
WPI; 98-481206/41.
                                                                                                                                                                                                               V84530 standard; DNA; 472 BP.
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Proceder A. Carter K.C. Dillon PJ. Enber R. Dances GA.

Pan P. Feng P. Ferrie K.C. Dillon PJ. Enber R. Dances GA.

Plorence K. Greene JM. Hi J. Kyaw H. Lafleur DM.

Li Y. Moore PA. Ni J. Olsen HS. Rosen CA. Ruben SM.

Li Y. Soppet DR. Wei Y. Young P. Yu G., Zeng Z.

BR Wil; 99-053885/05.

P. PEDBE: W88653, W88951.

P. PEDBE: W88653, W88951.

P. Wew isolated human genes and the secreted polypeptides they encode - to defend human genes and treatment of e.g. cancers. neurological disorders. immune diseases, inflammation or blood disorders.

PR J. 199-053885/05.

P. Dance J. D
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Epitopes; pollen; food allergy; Fageles; IgE antibodies;
hyposensitisation; ss.
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05-SEP-1997: US-057763.
05-SEP-1997: US-057764.
05-SEP-1997: US-057774.
05-SEP-1997: US-057774.
05-US-05774.
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Best Local Similarity 89.1%; Pred. No. 2.64e-05;
Matches 41; Conservative 2; Mismatches 3.
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/note= "birch P14"
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09-AUG-1991; EO1513.
13-AUG-1990; AT-001685.
11-APR-1991; US-683832.
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US-048915.
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US-048964.
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US-049375.
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US-057635.
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US-048901.
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US-057667.
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US-048971.
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06-JUN-1997;
05-SEP-1997;
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                       Homo sapiens.
W09854963-A2.
                                                                       04-JUN-1998;
18-DEC-1997;
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05-SEP-1997;
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06-JUN-1997;
                                                        10-DEC-1998.
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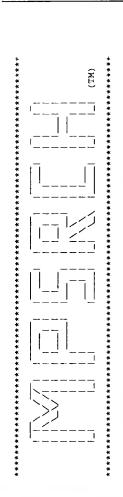
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Gaps 0;

Length 472, 3; Indels

Search completed: Sat Oct 23 22:08:20 1999 Job time: 401 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn Sat Oct 23 22:08:38 1999; MasPar time 126.78 Seconds 1191.820 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-5 (1-1747) from US08702718.seq 1747 Description: Perfect Score: N.A. Sequence:

TABLE default Scoring table:

Gap 6

165359 seqs, 43243793 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD:

Post-processing: Minimum Match 0% Listing first 45 summaries

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1 Database:

Mean 9.068; Variance 5.849; scale 1.550 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Res	Result No.	Score	Query Match	Query Match Length	DB	ID	Description	Pred. No.
;	-	48	2.7	7218	2	US-08-232-	Sequence 14, Applicati	7.31e-13
U	7	47	7.7	7218	CA	US-08-232-	14.	2.536-12
	m	40	2.3	700	~	US-07-846-	1, A	1.72e-08
	4	40	2.3	700	П	US-08-469-	7	1.72e-08
	'n	40	2.3	1046	Н	US-08-361-	Sequence 4, Applicatio	1.72e-08
	9	40	2.3	1046	m	US-08-484-	Sequence 4, Applicatio	1.72e-08
	7	40	2.3	1080	<b>.</b>	US-08-225-	-1	1.72e-08
	00	41	2.3	3933	4	PCT-US95-0	Sequence 1, Applicatio	5.00e-09
	6	41	2.3	3933	Н	US-08-199-	ř	5.00e-09
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	11	40	2.3	7859	m	US-08-450-	Sequence 15, Applicati	1.72e-08
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	13	38	2.2	84	m	US-08-664-	3,	1.98e-07
	14	38	2.2	85	Н	US-08-120-	97,	1.98e-07
	15	38	2.2	85	m	US-08-478-	Sequence 97, Applicati	1.98e-07
ပ	16	38	2.2	350	Н	US-08-171-	Sequence 14, Applicati	1.98e-07
	17	39	2.5	836	m	-869-80-SD	Sequence 7, Applicatio	5.85e-08
	18	39	2.2	880	e	US-08-616-	Sequence 7, Applicatio	5.85e-08
	19	39	2.2	1454	m	US-08-713-	Sequence 7, Applicatio	5.85e-08
	20	38	2.2	1978	S	5188642-3	Patent No. 5188642.	1.98e-37

1.98e-07 2.20e-06 2.20e-06	6.63e-07 6.63e-07 6.63e-07 2.20e-06	6.63e-07 2.20e-06 2.20e-06	2.20e-06 2.20e-06 6.63e-07	6.63e-07 2.20e-06 2.20e-06	6.63e-07 6.63e-07 2.20e-06	2.20e-06 2.20e-06 6.63e-07	6.63e-07 6.63e-07 6.63e-07
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Sequence 2, Sequence 28, Sequence 28,	Sequence 26, Sequence 37, Sequence 34, Sequence 15,	362	m C1 m	21	Sequence 17, Sequence 17, Sequence 1,	Sequence 94 Sequence 94	Sequence 1, Sequence 1, Sequence 1, Sequence 1,
-07-867 -08-151 -08-153	US-08-702- US-08-686- US-08-686- PCT-US93-0	US-08-104- US-08-798- US-08-314-	US-07-920- US-08-086- PCT-US91-0	US-07-688- US-08-384- US-08-444-	യയസ	US-08-453- PCT-US93-1	PCT-US95-0 US-08-280- US-08-457-
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22 23 23	25 25 26 27	30 30 30 30	337 337	3.54 3.54	1 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	044	4444

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COMPUTER: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFTMING SYSTEM: PC-DOS/MS-DOS
OFFTWARE: PatentIn Release #1.0, Version #1.25
                                                                         GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAS: (703)883-4109
TELEEX: 899140
AUDHESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AGG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                       Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                       XXXXXX
 RESULT
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                                                                                                                                                                                                                                  64 CGAGCCATGGTGTTCTATCGCGGCGTTTCTCTGCTGTCAAAGCTGCGTTCTCGAGCGGTC 123
                                                                                                                              Gaps
                                                                                                                                                                               4 CTTGGGATCTATTTCCTCTCTCTATTTCTCCCTAGGTAAAAGTTAATTTGTTGATTTTTT 63
                                                                                                                             o,
                                                             CLONE: PIZ9Pt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                2.7%: Score 48; DB 2; Length 7218; Similarity 3.6%; Pred. No. 7.31e-13; 7, Conservative 113; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
COPRESPONDENCES: 52
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30472/114 IMMU
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US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP 91 114 300.6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 3047:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEFAX: 899149
INFORMATION FOR SEC ID NO: 14:
SEQUENCE CHAPACTEPISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
LENGIH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER:
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Best Local Similarity
                                               IMMEDIATE SOURCE
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                                       TOPOLOGY:
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                                                                                                                              Matches
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Gaps 0;
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                                                                                                                                                                                                                                                            374 CCCCGAAAGCGAATTCCTTCATCGGGGTCAAGTAATGAGGTTTCCCACAGAAATGCTGTC 315
                                                                                                                                                                                                                                                                                                                                                                            314 ATTCCTCTCTCATTCCACCAAGAACCATATCAACTGTGATGTTTCCCAATTGAACCTTTCCA 255
                                                                                                                                                                                                                                                                                                                                                                                                                        254 IGCICTGACITGTAGGCGAICCTGTIGTICTGGAATCAATTCTTGCAGCTC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Valenta, Rudolf
APPLICANT: Valenta, Michael
APPLICANT: Duchene, Michael
APPLICANT: Pettenburger, Karin
APPLICANT: Kraft, Dietrich
APPLICANT: Rumpold, Helmut
APPLICANT: Scheiner, Otto
TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
TITLE OF INVENTION: and Therapy of Allergic Diseases
                                                                                                                                          0,
                                                                     CLONE: pTZgpt-Fls
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                Length 7218;
                                                                                                             Match 2.7%; Score 47; DB 2; Length 7218; Local Similarity 4.3%; Pred. No. 2.63e-12; es 13; Conservative 160; Mismatches 126, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Pelease #1.0, Version #1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-846-992-1 STANDARD; DNA; UNC; 700 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/353,844
FILING DATE: 18-MAX-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jones III, Harry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUTURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/846,992
FILING DATE: 19920606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/07846992
Sequence 1, Application US/07846992
Patent No. 5583046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jones III, Harry C
REGISTRATION NUMBER: 20,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
             TYPE: nucleic acid
STRANDEDNESS: single
                                         TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                 Ouery Match
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                                                                                                                                             Matches
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GENERAL INFORMATION:
APPLICANT: De Gree
                                                                               HYPOTHETICAL: NATI-SENSE: NO
                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Duchene, Michael
APPLICANT: Duchene, Michael
APPLICANT: Pettenburger, Karin
APPLICANT: Breitenbach, Michael
APPLICANT: Rumpold, Helmut
APPLICANT: Schoiner, Otto
TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
TITLE OF INVENTION: and Therapy of Allergic Diseases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             ö
                                                                                                                                                                          Score 40; DB 1; Length 700;
                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALP: 1003-271.

CARPUTER: READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
COMPUTER: TBM FC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/469,555
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/846,992
FILING DATE: 06-JUN-1992
APPLICATION NUMBER: US/07/846,992
FILING DATE: 18-WAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      ORGANISM: Betula verrucosa
IMMEDIATE SOURCE:
SEQUENCE 700 BP; 212 A; 127 C; 181 G; 180 T; 0 OTHER.
                                                                                                                                                                                                                           Pred. No. 1.72e-08;
                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                               T 4
US-08-469-555-1 STANDARD; DNA; UNC; 700 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6530-011
REFERENCE/DOCKET NUMBER: 6530-011
       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CARACTER.ESTICS:
LENGTH: 700 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08469555
Sequence 1, Application US/08469555
Patent No. 5648242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jones III, Harry C
REGISTRATION NUMBER: 20,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Valenta, Rudolf
                                                                                                                                                                          Query Match 2.3%;
Best Local Similarity 97.6%;
                                                                                                                                                                                               41; Conservative
                                                                                                    CDNA
                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNP
                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                               ORIGINAL SOURCE:
                                                                                                            HYPOTHETICAL: NAMI - SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: STATE:
                                                                                                                                                                                                                                                                                 XXXXXX
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0; Gaps
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APPLICANT: Van Ermelo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria-Helena
APPLICANT: Van Montagu, Marc
TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
TITLE OF INVENTION: EMBRYOS
                                                                                                                                                                                                                                                                                                                                       LIBRARY: POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN SEQUENCE 700 BP; 212 A; 127 C; 181 G; 180 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                            Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1; LA Pred. No. 1.72e-08; 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,467B
FILING DATE: 22-DEC-1994
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
APPLICATION NUMBER: EP 89 402 224.3
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US-08-361-467B-4 STANDARD; DNA; UNC; 1046 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Schulman, Robert M.
REGISTRATION NUMBER: 31,196
REFERNCE/DOCKET NUMBER: 010830-027
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08361467B Sequence 4, Application US/08361467B Patent No. 5633441
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNEB
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                           ORGANISM: Betula verrucosa IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: United States
ZIP: 22313-140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                              LENGTH: 700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.3%;
Best Local Similarity 97.6%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
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TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
TITLE OF INVENTION: EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Length 1046;
Pred. No. 1.72e-08;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,332C
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
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US-08-484-332C-4 STANDARD; DNA; UNC; 1046 BP
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APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
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REGISTATION NUMBER: 31,196
PEFERNCE/POCKET NUMBEP: 010830-093
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 4:
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APPLICATION NUMBER: US 08/361,467
ELLING DATE: 22-DEC-1994
PRIOR APPLICATION DATA:
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De Oliveria, Dulce E.
De Souza, Maria-Helena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08484332C Sequence 4, Application US/08484332C Patent No. 5767374
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS.
LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: De Greef, Willy
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COUNTRY: United States
ZIP: 22313-1404
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.3%;
Best Local Similarity 87.0%;
Matches 47; Conservative
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CLONE: 3C9
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APPLICANT:
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                                                                                                                                    Length 1046;
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                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
SEQUENCE 1080 BP; 229 A; 281 C; 359 G; 211 T; 0 OTHER.
                                                                                                          SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: YU, ET AL.

IITLE OF INVENTION: Superoxide Dismutase-4
NUMBER OF SEQUENCES: 16
CORRESPONDENCE STATEMENT OF ALCHERS ADDRESSEE: CARELLA, BYPNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                 Query Match 2.3%; Score 40; DB 3; L
Best Local Similarity 87.0%; Pred. No. 1.72e-08;
Matches 47; Conservative 0; Mismatches 7
                                                                                                                                                                                                                                                                       US-08-225-757B-1 STANDARD; DNA; UNC; 1080 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET VUMBER: 325800-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,757B
FILING DATE: 11 APR-94
                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08225757B Sequence 1, Application US/08225757B Patent No. 5506133 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 BECKER FARM ROAD
                                                                 MOLECULE TYPE: CDNA to mRNA IMMEDIATE SOURCE: CLONE: 3C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FERRARO, GREGORY D. REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1080 BASE PAIRS
                         nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEIC ACID
EDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6 BECKER FAR
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
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                                                      linear
                                       STRANDEDNESS:
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RESULT
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LOCATION: 126..179
SEQUENCE 3933 BP; 938 A; 1062 C; 1074 G; 859 T; 0 OTHER.
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Novel integrin alpha subunit NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSEE: Wolf, Greenfield and Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/02044
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: DETEMBLE CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/199,776
FILING DATE: 18 February 1994
ATTORNEY/AGENT INFORMATION:
NAME: Plumer' Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-720-3500
TELECAX: 617-720-3441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3933 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PCT-US95-02044-1 STANDARD; DNA; UNC; 3933 BP.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      Sequence 1, Application PC/TUS9502044 Sequence 1, Application PC/TUS9502044 GENERAL INFORMATION:
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CELL TYPE: mucosal lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
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LOCATION: 180..3659
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126..3662
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ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
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STATE: MA
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LOCATION:
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                   XXXXXX
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APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: NO. 5594120el integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.3%; Score 41; DB 1; Length 3933
Best Local Similarity 90.2%; Pred. No. 5.00e-09;
Matches 46; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: sig_peptide
LOCATION: 126..179
SEQUENCE 3933 BP; 938 A; 1062 C; 1074 G; 859 T; 0 OTHER.
                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
                                                                                                                                                ADDRESSEE: Wolf, Greenfield and Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JT 10
US-07-854-596B-4 STANDARD; DNA; UNC; 7859 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 B0801/7020
                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/07854596B Sequence 4, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION:
Sequence 1, Application US/08199776
Sequence 1, Application US/08199776
Patent No. 5594120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
CELL TYPE: mucosal lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dawson, Keith M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
180..3659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126..3662
                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
                                                                                                                                                                                 Boston
                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02210
                                                                                                                                                                                                    Ā
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                 / Match 2.3%; Score 40; DB 1; Length 7859; Local Similarity 81.3%; Pred. No. 1.72e-08; nes 52; Conservative 0; Mismatches 12; Indels
                                                                       COUNTY: USA

ZIP: USA

ZIP: 0606

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-JUN-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Stem Cell Inhibiting Proteins NUMBER OF SEQUENCES: 178
NUMBER OF SEQUENCES: 178
ADDRESSEE: HALE and DORR
STREET: 60 State Street
APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
CORRESPONDENCE ADDRESS:
                                         ADDRESSEE: Dr. John J. McDonnell
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7. 11
US-08-450-905B-15 STANDARD; DNA; UNC; 7859 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/08450905B Sequence 15, Application US/08450905B Patent No. 5856301 GENERAL INFORMATION:
                                                                                                                                                                                              92,337
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:

NAME: MCDONNell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,33
TELCOMMUNICATION INFORMATION:
TELEFAN: 312-715-1000
TELEFAX: 910-221-5317
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7859 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..7859
                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 TOPOLOGY: circular MOLECULE TYPE: CDNA
                                           Abba.
STREET: 1e..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 60 Sta
CITY: Boston
STATE: MA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    5638 AAAA 5641
                                                                                                                                                                                                                                                                                                                                                                                                                                    1744 AAAA 1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xxxxxx
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Sequence 3, Application US/08738367
Sequence 3, Application US/08738367
Sequence 3, Application US/08738367
Sequence 3, Application US/08738367
Sequence 3, Application US/08738367
Sequence 3, Application US/08738367
Sequence 3, Application US/08738367
Sequence 3, Application US/087367
Sequence 3, Application 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: DNA
SEQUENCE 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 12; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 3; Louis Pred. No. 1.72e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31,321
FR: 102.378.120DV-2
                                                                                     SOFTWARE: PATEBLIA MATERIA CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/450,905B
FILING DATE: 26-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/98,759
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
FILING DATE: 23-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
ATTONREY, FAGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REFERENCE/POCKET NUMBER: 1102.378.120
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SECONO
INFORMATION FOR SEG 1D NO: 15:
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US-08-738-367-3 STANDARD; DNA; UNC; 84 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 7859 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 8/ Cambridge
CITY: Cambridge
STATE: Massachusetts
COUNTR: U.S.A.
7.TP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 2.3%;
Local Similarity 81.3%;
hes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 7859 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5638 AAAA 5641
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APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Bowman, Michael
APPLICANT: Seudlding, Vikki
APPLICANT: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       ö
                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                    Length 84;
                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,596B
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367 FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                         Score 38; DB 3; Le
Pred. No. 1.98e-07;
0; Mismatches 3.
                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE 84 BP; 76 A; 0 C; 0 G; 7 T; 1 OTHER.
                                                                                                                                                                                                                                                                       .r 13
US-08-664-596B-3 STANDARD; DNA; UNC; 84 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge CITY: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08664596B Sequence 3, Application US/08664596B Patent No. 5807703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                        ATTORREYAGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 498-8224
TELEPAN: (617) 848-824
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
McCoy, John
LaVallie, Edward
                                                                                                                                                                                   Query Match 2.2%;
Best Local Similarity 93.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
UNMBER OF INVENTION: 101
CORRESPONDENCE: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.2%; Score 38; DB 1; Length 85; Best Local Similarity 88.0%; Pred. No. 1.98e-07; Matches 44; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                      3; Indels
                                                                                                                                                      Score 38; DB 3; Length 84;
Pred. No. 1.98e-07;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: SASTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
FILLING DATE: 15-SEP-1993
                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE 85 BP; 50 A; 5 C; 10 G; 20 T; 0 OTHER.
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE 84 BP; 76 A; 0 C; 0 G; 7 T; 1 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24,618
ep. 714-158-0 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1, 135
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ODIOn, NO. 5525455man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 714-158-
TELEPHONE: (703)413-3000
TELEPHONE: (703)413-220
TELEPHONE: (703)413-220
TELERAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO. 97:
SEQUENCE GRARACTERISTICS:
LENGTH: 85 Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                  JT 14
US-08-120-827-97 STANDARD; DNA; UNC; 85
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97, Application US/08120827
Sequence 97, Application US/08120827
Patent No. 5525463
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEENE, JACK D.
KING, PETER H.
                                                                                                                                                           Query Match 2.2%;
Best Local Similarity 93.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USBFUL IN THE
TITLE OF INVENTION: PECCENITION, BINDING AND EXPRESSION OF PIBONUCLESS ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGILATION
UNMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
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0
                                                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 175 Jefferson Davis Highway, Fourth Floor CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.2%; Score 38; DB 3; Length 85; Best Local Similarity 88.0%; Pred. No. 1.98e-07; Matches 44; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATION OF PACHION Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,675
FILING DATE: 07-JUN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,827
ATOMNEY/AGENT INFORMATION:
ANAMER: 15-SEP-1993
ATOMNEY/AGENT INFORMATION:
ANAMER: US 08/120,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: CDNA
SEQUENCE 85 BP; 50 A; 5 C; 10 G; 20 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ODION, NO. 5773246man F.
PEGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
   JT 15
US-08-478-675-97 STANDARD; DNA; UNC; 85 BP.
                                                                Sequence 97, Application US/08478675
Sequence 97, Application US/08478675
Patent No. 5773246
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                       XXXXXX
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Search completed: Sat Oct 23 22:10:49 1999 Job time: 131 secs.

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(MI)	
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	
<pre>4Psrch_nn n.a n.a. database search, using Smith-Waterman algorithm</pre>	
Run on: Sat Oct 23 21:11:35 1999; MasPar time 2958.33 Seconds 1383.723 Million cell updates/sec	s/sec
•	
<pre>fitle: &gt;US-08-702-718-5 Description: (1-1747) from US08702718.seq</pre>	
uence: 1 GCTCTTGGGATCTATTTCCTAAAAAAAAAAAAAA	AA 1747 FT
Scoring table: TABLE default Gap 6	
Nmatch STD : Dbase 0; Query 0	
Searched: 2883791 seqs, 1171580779 bases x 2	
Post-processing: Minimum Match 0% Listing first 45 summaries	
obtabase: 6	
statistics: Mean 12.404; Variance 6.933; scale 1.789	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	pa,

## 8.2 522 10 #A237580 mx11d01.rl Soares mous 5.69e-74 7.7 501 11 #A313713 EST15581 Colon carcin 1.42e-67 7.5 213 12 #A238915 GH15054.5prime GH Dross 4.14e-59 7.0 540 24 A1238915 GH15054.5prime GH Dross 4.14e-59 7.3 14 #A498291 vh38911.rl Barstead mo 2.08e-58 7.2 443 14 AA24510 mx08910.rl Soares mous 9.83e-51 7.0 5.3 509 9 AA112941 mx08910.rl Soares mous 9.83e-51 7.0 5.8 444 10 AA24510 mc66602.rl Soares mous 9.83e-51 7.0 5.8 444 10 AA24510 mc66602.rl Soares mous 9.83e-51 7.0 5.8 444 10 AA24510 mt16h01.rl Soares mous 9.83e-51 7.0 5.8 444 10 AA24510 mt16h01.rl Soares mous 9.83e-51 7.0 5.8 509 9 AA17872 mt16h01.rl Soares mous 9.83e-51 7.0 5.8 499 23 A118724 mt23d11.rl Soares mous 9.83e-51 7.0 5.8 499 23 A118729 cc58d01.sl Soares mous 9.83e-51 7.0 5.8 510 21 G88687 mt26d1.sl NGI_GGAP_GC 3.29e-45 7.0 5.8 510 21 G88687 mt26d1.sl NGI_GGAP_GC 3.29e-45 7.0 5.8 510 AA568724 mg2169.sl NCI_GGAP_GC 3.29e-45 7.0 5.6 513 AA427173 vc83c01.sl NCI_GGAP_GC 3.29e-45 7.0 5.6 513 AA337328 mp70f10.xl Soares mous 7.77e-44 7.5 52 53 A1327328 mp70f10.xl Soares mela 4.22e-41 7.5 52 54 53 A1327328 mp70f10.xl Soares mela 4.22e-41 7.5 52 54 53 A1327328 mp70f10.xl Soares mela 4.22e-41 7.2 52 54 53 A1327328 mp70f10.xl Soares mela 4.22e-41 7.2 52 54 53 A1327328 mp70f10.xl Soares mela 4.22e-41 7.2 52 54 53 A1327328 mp70f10.xl Soares mela 4.22e-41 7.2 52 54 53 A1327328 mp70f10.xl Soares mela 4.22e-41 7.2 52 54 54 55 54	ALIGNMENTS  ALIGNMENTS  895953  471 bp mRNA  20-38673 Ice plant Lambda Uni-Zap XR expression library, 30 ho acl treatment Mesembryanthemum crystallinum cDNA clone L30-386 miniar to Citrate synthase, mitochondrial precursor, mRNA 896953  8896953  Grand
00 00 101 111 111 111 111 111 111 111 1	RESULT 1 LOCUS DEFINITION ACCESSION NID VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT
<del></del>	

130-386T3 Ice plant La 9.20e-150 7448 Lambda-PRL2 Arabi 1.67e-122 C96653 Rice callus Ory 6.97e-108 16899 Lambda-PRL2 Arab 1.07e-105 AU00269 Bombyx mori p 1.07e-105 EST220465 Normalized r 2.94e-96 16916 Lambda-PRL2 Arab 8.24e-95 vm94409.rl Knowles Sol 2.60e-88 ccau00002614 Cotton Bol 1.48e-82 CDC534.R cDNA from oat 2.10e-80

AA896953 T44185 C96653 R90544 AU002699 AI176862 R90561 AA054878 AA054878

471 20 502 17 417 24 478 31 620 26 676 23 527 31 5657 15

247 210 1190 1187 1172 1172 1153

υ

Pred. No.

Description

SUMMARIES

% Query Score Match Length DB

Result No.

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Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; eukaryota; Viridiplantee; Streptophyta; eudicotyledons; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Roslade; Capparales; Brassicaceae; Arabidopsis.

1 (bases; Lo 502)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., Monttosh, L., Ohlroqge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, Of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
                                                                                                                                                                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             973 TTAGCTGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGCTATGGATCAAATCTGTT 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 TTAAAAAGTGGCAAGGTTGTACCTGGATATGGCCATGGAGTTCTGCGCAAGACGGATCCA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 CTGGTTTCGAAGCTGTATGAATGGTGCCTCCAATTCTGACAGAGCTTGGGAAGGTAAAGA 362
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DEFINITION 7448 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123C9T7, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AGATACTCTTGCCAGAGGGACTTTGCCCTTAAGCACTTACCTAATGATCCACTATTTCAA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CATTIGGIGGIAGCGCACTTTCAGAICCTTACCTTTCATTIGCAGCIGCACTGAAIGGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                             /db_xref="taxon:3344"
/clone="Laxon:3344"
/clone="Laxon:386"
/clone=lib="ce-plant Lambda Uni-Zap XR expression
library, 30 hours NaCl treatment"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/dev_stage="Six week old"
/dev_stage="21" t 12" t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GTGGATGAATGTGGAGAAAACATCAGCACGGAGCAGCTAAAAGATTATGTCTGGAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 247; DB 20; Length 471; Pred. No. 9.20e-150;
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                                                                                                                                 /organism="Mesembryanthemum crystallinum"
High quality sequence stop: 320.
Location/Qualifiers
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Arabidopsis thaliana
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Best Local Similarity 80.3%;
Matches 354; Conservative
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                                                                                              SOUTOR
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/ortall variation and a supplied of the many sources were lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNN. The mRNA sources were l) 7 quantities of 6 4 pools of mRNN. The mRNA sources were l) 7 day germinated etholated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oilgo dr primed CDNA. [Ab_xref="faxon:3702"]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 ATGGTTTAGCTGGCCACTCCATGGTTTGGCTAATCAGGAAGTTTTGCTTTTGGATCAAAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 CAGTCGTAGAGGAATGTGGAGAGATATATCAAAAGAACAGTTGAAAGAATATGTTTGGG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 CTGGICACCTGGTTGGTAGTGCACTTTCAGACCCATATCTGTCATTTGCAGCTGCATTAA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 1GGATTATGGTGCAAATTTTTCCCACATGTTGGATTTGATGATGAAAAGGTGAAAGGAC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 AAACATTAAACAGTGGCAAGGTTATTCCGGGGTATGGTCACGGTGTTCTNCGCAATACT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-0CT-1998
                                                                        MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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DEFINITION C96653 Rice callus Oryza sativa cDNA clone C10531_5A, mRNA
On Jan 7, 1998 this sequence version replaced gi:948518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.67e-122;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/strain="var columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 210; DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="123C9T7"
/clone_lib="Lambda-PRL2"
90 c 118 g 149
                                                                                                                                                                         Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seg primer: T7
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                    Contact: Thomas Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.0%;
Best Local Similarity 79.1%;
Matches 284; Conservative
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Poaceae; Oryza.

MEDLINE

US-08-702-718-5.rst

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lambda-PRL2"
90 c 113 q 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="var columbia"
                                                                                                                                                                                                                                                                                                                                  Tel: 577-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: 17 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                  Contact: Thomas Newman
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1 Similarity 79.3%;
265; Conservative
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                                                                                                                                                                                                                                                                                                                               /strain="cultivar Nipponbare, sub_species Japonica"
/note="Vector: plauescript II SK+; Site_1: Sall; Site_2:
Not1: cDNA prepared from rice callus mRNAs by using
oligo(dT) a primer and ligating to the Sall-NotI site
of pBluescript II SK+ phagemid. "
/db_xref="taxon:4530"
/map="ll"
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16899 Lambda-PRL2 Arabidopsis thaliana cDNA clone 189D15T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    793 TAIGGIGCAAATITIGCICACAIGCIIGGITICAGIAGCICIGACAIGCAIGAGCIIAIG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853 AAGCTCTATGTCACGATACACAGTGATCATGAAGGTGGTAACGTCAGTGCTCACACAGGT 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 ITAGCIGGACCATIGCACGGCCTGGCTAATCAGGAAGTGCTGTTGTGGAATCAAATCTGTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 ATAGGIGAGACAGGIAGIGATGITACAACIGAICAACICAAAGAGIAIGIGIGGAAGACA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TATGCAGCAAACTITTCACACATGCTTGGGTTTGATGATCCCAAAATGCTCGAGTTGATG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CGACTATATGTGACAATCCACACTGATCATGAAGGTGGAAATGTCAGTGCTCATACTGGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TATGTTTACCGGAGGATCTTCAAGGATGGGAAAACTATAGCAGCTGATAATGCACTGGAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 110; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1093 IIGAAAAGTGGCAAGGTIGTCCCGGTTTCGGACATGGAGTTCTGCGCAAGACTGAT 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 CATCTGGTTGGAAGTGCTCTGTCAGATCCTTATCTTTTTGCAGCTGCACTGAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 190; DB 24; Length 417; Pred. No. 6.97e-108;
                                                                  On Aug 21, 1998 this sequence version replaced
                                                                                                      Contact: Takuji Sasaki
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="C10531_5A"
/clone_lib="Rice callus"
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                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
                                                                                                                                                                                                                                            Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                       Rice Genome Research Program 2-1-2 Kannondai, Tsukuba
1 (bases 1 to 417)
Sasaki,T. and Minobe,Y.
Rice cDNA from callus
Unpublished (1994)
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Matches 306; Conservative
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R90544.1 GI:958084
                                                                                                                                                                                                         Tel: 0298-38-7441
Fax: 0298-38-7468
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/note-"vector: lammda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNN. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and sliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using colling of Tprimed cDNA.

/clone-"18991517"
Arabidopsis thaliana
Eukaryota; Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledons:
Rosidae: Capparales; Brassicaceae: Arabidopsis.
1 (bases 1 to 478)
Newman,T., deBruilin,F.J., Green,P., Keegstra,K., Kende,H.,
McThtosh,L., Ohlrogge,J., Raikhel,N., Somerville,C.
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant, Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 ITTGCCTTGAAGCATCTACCTGACGNCCCTCTTTTCCAGCTGGTGTCAAAGCTTTATGAA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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Pred. No. 1.07e-105;
0; Mismatches 67;
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AI176862.1 GI:3727500
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Best Local Similarity 67.0%;
Matches 370; Conservative
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                  AU002699 Bombyx mori p50(Daizo) Bombyx mori cDNA clone n0357, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 TCCAAAGAGCAGTTGAAAGACTACGCTTGGAAAACATTGAAAAGTGGCAAGGTTGTCCCT 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1177 GCTTTGAAGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTGCAAAACTCTACGAAGT- 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GGTTACGGTCATGCAGTACTTAGAAAACTGATCCAAGATATACTTGCCAGCGTGAGTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 CATTCGGGAGTTCTTTTGCAGTATTATGGTCTGAAGGAGATGAACTACTATACAGTAATG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       877 GAICAIGAAGGIGGIAACGICAGIGCICACACAGGICACTIGGIIGCIAGIGCIIIGICA 936
15-JAN-1999
                                                                                                                                                                           Eukaïyota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Petryqota; Lepidoptera; Bombycoidea; Bombycidae; Bombyx. 1 (bases 1 to 620)
Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Establishment of CDNA database of Bombyx mori Unpublished (1999) on Sep 1, 1995 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACCACGAGGGTGGAAACGTTTCTGCGCACAACGCATTTAGTGGGTTCTGCTCTTAGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 191; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 187; DB 26; Length 620; Pred. No. 1.07e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"Bombyx mori p50(Daizo)"
141 c 146 g 171 t
                                                                                                                                                                                                                                                                                                                                  Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
PROJECT = 'CREST project by JST',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="n0357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                 AU002699.1 GI:4159092
620 bp
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Best Local Similarity 67.1%;
Matches 396; Conservative
                                                                                                                                        domestic silkworm.
                                                                                                                                                            Bombyx mori
                                         sequence.
                                                         AU002699
                                                                          94159092
                  DEFINITION
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JOURNAL
COMMENT
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All76862 676 bp mRNA EST 20-JAN-1999
ST21220465 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROYBX80 3' end, mRNA sequence.
All76862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1374 AAGAGCICITGAIACACCAAAGAGGACCGIAIAATATCTTGCTTCAGTTAAACCATAATA 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 CTGGAGCACCACCCACTGTGAGCATCTACGTTGGGCCAGGGGTTCTTAGCCTTTCCTTG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 CTCTAAGAGGATATTGGGCACAATCTTGTACAGCTGAGCAACCAGCTTAAACATGGGGATC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 CTTGGGCAGATGTTTCAGAGCAAACTCTCGCTGACAGGAATATCGTGGATCAGTCTTCCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 TAGGACTGCATGACCATATCCTGGGACAACCCGTCCCGAGTTGAGTGTGTTTCCAGATGTA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: ovary; Vector: pT7T3Pac; Site_1: ECORI; Site_2: Not1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 CTTGGGCCTTTCTAGAGGGAAGCCTAGGGCTCTGCTCCAGATAAGCTGGGCCAACACACC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 CAGTGCCCTCGACACTCCGAACAGGACTGTGTAGTAATTCATCTCCGTCATGCCATAGTA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 174; DB 23; Length 676;
Pred. No. 2.94e-96;
0; Mismatches 179; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 676)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jan 19, 1998 this sequence version replaced gi:2152042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Normalized rat ovary, Bento Soares"
188 c 150 g 181 t 1 others
The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="ATCC (inhost):2031570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus sp."
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/clone-"ROVBX80"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kerlavage, A.R. and Adams, M.D.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes; Spermatophyta, Magnoliophyta, eudicotyledons;
Rosidae, Capparales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 527)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrugge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R90561 527 bp mRNA EST 30-DEC-1997
16916 Lambda-PRL2 Arabidopsis thaliana cDNA clone 18943T7, mRNA
                                                                                    1077 GICTITICAACIGCICTITIGGAAAIGIICICCCCACACTCCTCTACAACAGATITIGAICCA 1018
483 GICTCGTAACTICTCATCTGACACGTCTTTGCCGACTTCCTTCTGTAGCTGCGTCAGCCA 542
                                                                                                                                                                         543 GACAAGCACCTCCTGGTTTGCTAGTCCATGCAGAGGCCCTGCCAGCCCATTCATAGCTGC 602
                                                                                                                                                                                                                 603 IGCANAGGACAGGIAAGGGICIGAAAGGGCGCIGCCCACCAAGIGGCTIGIGIGGGGCACT 662
                                                                                                                                                                                                                                                                                                                                                                                           MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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/strain="var columbia"
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106 c 122 q 14:
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Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo dT primed cDNA. /db_xref="taxon:3702"
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Location/Qualifiers
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Best Local Similarity 76.7%;
Matches 247; Conservative
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Tel: 517-35
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cloned into the NotI/Sall sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 657)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="B6D2 F1/J"
/note="Organ: embryo; Vector: pSPORT; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally from mRNA prepared
from 800 blastcoysts. Primer: Sall(dT):
5'-CGGTCGACCGTCTTTTTTTTTTTTTTTT"3'. CDNAS were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA606966 657 bp mRNA EST 30-SEP-1997 vm94h09.rl Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:1005953 5' similar to SW:CISY_PIG P00889 CITRATE SYMTHASE, MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:570169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AGACTTGGCGAACCGTGCTGCTGTGCCAGATTATGTGTACAATGCCATGGATGCTTTGCC 187
                                                                                                                                                                                                                                                                          507 GGAATIGCGAAGTCGTGCTACTGTCCCCGATCATGTATACAAAACTATTGATGCCTTACC 566
                                                                                                                                                                                                                                                                                                                                188 ITCCACAGGTCCATCCAATGACTCAATTTGCTAGCGGTGTTATGGCCCTCCAGGTGCAAAG 247
                                                                                                                                                                                                                                                                                                                                                          248 TGAGTTTCAAAAGGCATATGAGAATGGAATTCATAAGTCAAAGTTCTGGGAGCCAACATA 307
                                                                                                          68 TTTGTGGCTTCTCTTAACTGGAAAGGTACCTAGCAAAGAGCAAGTTGAAGCACTGTCGAA 127
                                                                                                                                                               447 ICICIGGCIICITITAACAGGAAAGGIGCCAICAAAAGAGCAAGIGGAIICAIIGICICA 506
8 IGAGIGCCAGAAAGIAIIACCIACIGCCCAGICIGGAGCIGAACCAIIACCGGAGGGICI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1328460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washu'HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Technologies). Two difinserts) and B3."
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 TGAGGATIGCCICAACCIGATI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 IGAGGATICCAIGAGTTIGATI 708
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Fax: 314 286 1810
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KEYWORDS
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Clemson University Genomics Institute

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1 (bases 1 to 585)
Wan,C.-H., Yu,Y., Sasinowski,M. and Wing,R.A.
Cotton EST Database: Sequence Analysis of 2000 cDNA Clones from an
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1144 ACTGATCCAAGATACACATGCCAGAGAGTTGGCTTTGAAGCATTTGCCTGAAG-ATCC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1203 ACTGTTTCAA-CTGGTTGCAAAACTCTACGA-AGTGTTCCTCCAATTCTTACAGAACTTG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1319 ATGGTTTAACTGAAGCAAGATATTATACGGTCCTCTTTGGTGTATCAAGAGCTCTTGGCA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1024 AAATCTGTTGTAGAGGAGTGTGGGGAGAACATTTCCAAAGAGCAGTTGAAAGACTACGCT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1084 TGGAAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGCAAG 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        964 TIGAAIGGITIAGCIGGACCACIICAIGGIIIAGCCAAICAGGAAGIIIIGCIAIGGAIC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 ATGAATGGGCTGGCGGGCT-CTACATGGACTAGCAAATCAGGAGGTGCTTGTCTGGCTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 ACACAGCTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTTACGAGACTACATC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAACACACTCAATTCAGGACGGGTGGTCCCAGGATACGGTCATGCAGTACTGAGGAAG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 ACTGACCCTCGCTATTCCTGTCAGCGAGATTTGCTCTGAAACATCTGCCTAAGGGATTC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 CCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGCCCAATATCCTCTTAGAGCAAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 GGAAGGCTAAGAACCCTTGGCCCAACGTAGACGTCACAGTGGGGTGCTGCTCCAGTACT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 AIGCAIGACGGAGAIGAACIACIACAACAGICCIGIIIGGAGIGICICGGGCACIGGGIG 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIO54878 585 bp mRNA EST 16-JUL-1998 coau0002G14 Cotton Boll Abscission Zone cDNA Library Gossypium hirsutum cDNA clone coau0002G14 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                          904 CACACAGGTCACTTGGTTGCTAGTGCTTTGTCAGACCCTTACCTCTCCCTTCGCTGCTGCT 963
                                                                                                                                                                                                                                                                                                                                                                                   79 CACACAAGCCATTTGGTGGGCAGGGCATT-TCAGACCCTTACCTGTCCTTTGCAGCAGCC 137
                                                                                                                                                                                                                                                                                 19 GAGCTCATGCGTTTGTACCTCACCATCCATGTGACCATGAGGGTGGTAATGTAAGTGCC 78
                                                                                                                                                                          Score 163; DB 15; Length 657;
Pred. No. 2.60e-88;
0; Mismatches 192; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1379 TITGCTCTCAGCTAATITGGGACCGAGCTCTTGGATTGCCACTAGAGAGGSCAAAG 1434
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/clone_lib="Knowles Solter mouse blastocyst B1"
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                /tissue_type="blastocyst"
/dev_stage="embryo" (pre-implantation)"
/lab_host="bH10B" 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abscission Zone Library
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                                                                                                                                                                          ch 9.3%;
l Similarity 66.6%;
397; Conservative
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Gossypium hirsutum
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                                                                                                                                                                             Query Match
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Contact: Wing RA

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
Poaceae; Avena.
                                                                                                                                                                                                                                                                          /note="Vector: Uni-ZAP XR; Site_1: EcoRI, Site_2: XhoI; This is a Uni-ZAP XR custom cDNA library made by Stratagene (U.S.A.: 1-800-424-5444): Stratagene cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GCGATGGTGTTTTTGAAGGGAGTATCAGCGCTATCCAGTCTAAGGTCACGTGTTAAACAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 GCCATGGTGTTCTATCGCGGCGTTTCTCTGCTGTCAAAGCTGCGTTCTCGAGCGGCGTCCAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 CATICCAGICICAGCAAIICIGIIAGAIGGCIICAAAIGCAGICCICIICCGAICIIGAI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 CAGACAAATCTTAGCAACTCTGTGCGGTGGCTTCAAGTCCAAACCTCTTCTGGTCTTGAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 CTGCGTTCTGAGCTGCAAGAATTGATTCCAGAACAACAGGATCGCCTAAAGAAGCTCAAG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 TCAGAGCATGGAAAGGTTCAATTGGGAAACATCACAGTTGATATGGTTCTTGGTGGAATG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 AGAGGGATGACAGNGGTTGCTTTTGGGAAACCTCATTACTTG-CCCAGATGGGGGAATTCG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Cotton Boll Abscission Zone cDNA Library"
/lab.host="XLI-Blue MRF" 8 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Gaps
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VanDeynze, A.E., Sorrells, M.E., Park, W.D., Ayres, N.M., Fu, H., Cartinhour, S.W. and McCouch, S.R.
Anchor Probes for Comparative Mapping of Grass Genera Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA231705 307 bp mRNA EST 27-FEB-199
CDO534.R cDNA from oat Avena sativa cDNA clone CDO534, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 GCAGAACTGGNAAAAGTGCAACTTGGGAATATTACTGTTGATATGTGTCATTGGTGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 AGAGGAATGACAG-GATTACTGTGGGAAACCTCATTACTTGACCCCGGATGAAGGAATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 CTTTGGGGCCTTGTCATTCCGN-AGTGTCAAAAACTATTACCAGCTGCAAA-CCTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 CTTCATTCGCAGTTGAAGGAATTGATTCCTGAACAACAGGGGCGCCTGAAGAAACTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 155; DB 22; Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 97; Indels
                                                                                                    Email: rwing@clemson.edu
Seg primer: SP030 (AACAGCTATGACCATGATTA)
High quality sequence stop: 239.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

8.9%; Score 155; DB 22;
Best Local Similarity 73.7%; Pred. No. 1.48e-82;
Matches 291; Conservative 0; Mismatches 97
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Fax: 864 656 4293
                                                                                                                                                                                                                                                   /organism-"Gossypium hirsutum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 AGAACC-TI-CGINAGGGTCTI-TATGGCTTCTTT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 AGAGCCCTTGCCTGAAGGTCTTCTCTGGCTTCTTT 460
                                                                                                                                                                                                                                                                                                                                                                                       /db_xref-"taxon:3635"
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone-"coau0002G14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 9
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the Modified pT/T3 vector. Library constructed and normalized by Bento Soares and M.Fatima
1 (bases 1 to 522)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Besel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptee,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: mousesex@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 CTTACCTCTCCTTCGCTGCTGCTTTTGAATGGTTTAGCTGGACCACTTCATGGTTTAGCCA 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1001 ATCAGGAAGTITIGCIATGGATCAAATCTGTTGTAGAGGAGTGTGGGGGAGACATTTCCA 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1181 TGAAGCATTTGCCTGAAGATCCACTGTTTCAACTGGTTGCAAAACTCTACGA-AGTGTTC 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 ACGGTCATGCAGTACTGAGGAAGACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 CITACCIGICCTIIGCAGCAGCCAIGAAIGGGCIGGCGGGGCI-CIACAIGGACIAGCAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGGGTGGTAATGTAAGTGCCCACACACACATTTGGTGGG-AGCGCTGT-TCAGACC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 168; Indels 6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 TGAAACATCTGCCTAAGGATCCCATGTTCAAGCTGGTGGCTCAGCTGTACAAGATTGTGC
                                                                                                                                                                                        Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1392879
                                                                                                                                                                                                                                                                                             Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 143; DB 10;
Pred. No. 5.69e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
125 c 150 g 118 t
                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
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                                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 453,
Location/Qualifiers
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1 Similarity 66.6%;
347; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              // note="vector: Uni-ZAP XR/pBluescript; Site_1: EcoRI; Site_2: Xho1; A Uni-ZAP XR CDNA library was constructed from etiolated leaf mRNA from the oat cultivar 'Brooks' and converted to pBluescript (amp resistant) as described in Heun et al. (1991) Genome 34:437-447. For insert amplification, use Ml3 forward and revers: primers. Clones from this library are designated with the prefix 'CDO'. *Note: Clone CDO1081 was recloned into the TA cloning vector and carries kanamycin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1138 CGCAAGACTGATCCAAGATACACATGCCAGAGAGATTCGCTTTGAAGCATTTGCCTGAA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TGGATCAAATCTGTGATGGAAGAAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TACGTATGGAAGACACTGAAGAGGTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CGTAATACAGATCCACGATACTCGTGCCAAAGGGAGTTTGCACTTAAGTATTTACCCGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GACCCACTTTTCCAACTGGTCTCCAAGTTGTACGAAGTTGTGCCTCCTTACTGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCGGCACTGAACGGTTTAGCTGGGCCACTGCATGGCCTGGCTAATCAGGAAGTGTTGCTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                           Email: srm4@cornell.edu
cDNA from oat (Avena sativa); reverse sequence of RFLP probe
CDO534. Sequence determined by Nicola M. Ayres.
  On Nov 29, 1993 this sequence version replaced gi:634857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 152; DB 10; Length 30°
Pred. No. 2.10e-80;
0; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Brooks"
                                                                        Dept Plant Breeding
Cornell University
Thadaa, W 14833-1901, USA
Tel: 607 255 6683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA237580
91861602
AA237580.1 GI:1861602
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Best Local Similarity 75.6%;
Matches 232; Conservative
                                                       Contact: McCouch SR
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                                                                                                                                                                                                                                                                                                                        EST185581 Colon carcinoma (HCC) cell line Homo sapiens CDNA 5' end similar to similar to citrate synthase, mRNA sequence.
AA313713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
                                                                            1298 GIGGIGITGITGAACTATTAIGGITTAACIGAAGCAAGATATATACGGICCTCTTIG 1357
1240 CTCCAATTCTTACAGAACTTGGCAAAGTTAA--ACCCTTGGCCAAATGTTGATGCCCACA 1297
                                                 418 GTGGGGTGCTGCTCCAGTACTATGGCATGACGGAGATGAACTACTACACAGTCCTGTTTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI: Site_2: Moo!
/db_xref="ATCC (inhost):109839"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                     19-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:693326
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                                                                                                                                                                                                  1358 GIGTATCAAGAGCTCTTGGCATTTGCTCTCAGCTAATTTGG 1398
                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                  478 GAGTGTCTCGGGCACTGGGTGTGCTAGCCCAGCTCATCTGG 518
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/cell_type="KM12C"
                                                                                                                                                                                                                                                                                                        mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerlavage, AR
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217455 213 bp mRNA EST 10-NOV-1992 ATTS0029 AC16H Arabidopsis thaliana cDNA clone TAT2B1 5' similar to CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR. Swiss-Prot entry P00889,
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/strain-"ecotype Columbia
/note-"vector: Lambda ZaPI; tissue-cell suspension
culture of ecotype columbia; clone_library=ACI6H; Cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1135 CTGCGCAAGACTGATCCAAGATACACGCAGAGAGAGTTCGCTTTGAAGCATTTGCCT 1194
                                                                                                                                                                                                                                                                                 62 GTCTGGCTAACACAGCTGCAGAAGGAAGTTGGCAAAGATGTGTCAGATGAGAAGTTACGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GACTACATCTGGAACACACTCAACTCAGGACGGGTTGTTCCAGGCTATGGCCATGCAGTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 AAIGACCCCAIGITIAAGIIGGIIGCICAGCIGIACAAGAIIGIGCCCCAAIGICCTCIIA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 CAGTATTATGGCATGACGGAGATGAATTACTACACGGTCCTGTTTGGGGTGTCACGAGCA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 ITGGGTGTACTGGCACAGCTCATCTGGAGCCGAGCCTTAGGGTTCCCTCTAGAAAGGCCC 481
                                                                                                                                            2 GCAGCAGCCATGAACGGGCTGGCAGGGCCTCTCCATGGACTGGCAAATCAGGAAGTGCTT 61
                                                                             Gaps
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   DB 11; Length 501;
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BP 27,31326 Castanet-Tolosan cedex,France
Email: lescuredtoulouse.inra.fr.
Location/Qualifiers
                                        Pred. No. 1.42e-67,
       Score 134;
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7.78;
                                 Best Local Similarity 65.4%;
Matches 316; Conservative
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UMR05 CNRS/INRA
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Best Local Similarity 63.7%;
Matches 283; Conservative
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                                                                                                                                                                                  7
vector: Lambda ZAPII; Physiological condition: cycling
                                                                                                                                                                                                                                                                                                                                                                                        983 CACTICATGITITAGCCAAICAGGAAGITITGCIAIGGAICAAAICIGITGIAGAGGAGT 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION GH15054.5prime GH Drosophila melanogaster head pOT2 Drosophila ACCESSION AI238915
                                                                                                                                                                                                                                                                                                             923 CTAGIGCITIGICAGACCCTTACCTCTCCTTCGCTGCTGCTTTGAATGGTTTAGCTGGAC 982
                                                                                                                                                                                                                                                                                                                                                                   125 CACTCCATGGTTTGGCTAATCAGGAAGTTTTGCTTTGGATCAA-TCAGTCGTAGAGGAAT 183
                                                                                                                                                                                                                                                       65 GTAGIGCACTITCAGACCCATATCIGICATITGCAGCIGCATTAAAIGGITTAGCIGGGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilade; Drosophila.

( hases: 1 to 540.

Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 12A, Berkeley, CA 94720-3200, USA
Exa: 510 643 9947
Exa: 510 643 9947
Exa: 510 cov. E Column: 6
Plate: 150 row: E Column: 6
High quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                                                                                                         64
                                                                                                                                                                                    Gaps
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/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone="fqH1504"
/clone=lib="dH Drosophila melanogaster head porz"
/sex-"male and female"
/dev_stage="adult"
/db_host="host = 1pf 9 98 t
                                                                                                                                                                                  2;
                                                                                                                                                  Length 213;
                                                                                                                                                                                  0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Aug 21, 1998 this sequence version replaced
                                                                                                                                              Score 131; DB 8; 1
Pred. No. 1.89e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 GTGGAGAAGATATATC-AAAGAACAGTTGAA 213
                                  /db_xref="taxon:3702"
/clone="TAT2B1"
/clone_lib="AC16H"
40 c 52 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI238915.1 GI:3833773
                                                                                                                                            Query Match 7.5%;
Best Local Similarity 83.4%;
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Harvey, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .540
                     cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly.
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                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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7.0%; Score 122; DB 24; Length 540;

Query Match

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Eukaryotta: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 473)

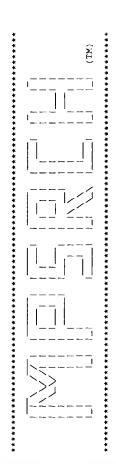
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS AA498291 473 bp mRNA EST 01-JUL-1997
DEFINITION Wh38911.r1 Barstead mouse pooled organs MPLRB4 Mus musculus CDNA clone INAGE: 889316 5' similar to SW:CISY_PIG P00889 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR ;; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1087 AAAACATTGAAAAGTGGCAAGGTTGTCCCTGGTTTCGGACATGGAGTTCTGCGCAAGACT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 AACGGICIGGCIGGICCCCIGCACGGCCIGGCCAACCAGGAGGIGCICGIGIGGCTGCGG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 AAGCTGCAGAAGGAGGCCGGCAACAACCCGTCGGAGGAGCAGCTCAAGGAGTACATCTGG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 AAGACCCTCAAGTCCGGACAGGTGGTTCCCGGCTACGGACACGCCGTGCTCCGCAAGACC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 GATCCCCGCTACACCTGCCAGCGTGAGTTCGCGCTGAAGCACCTGCCCGAGGACGAGACG 516
                                                                                           CTGGATTGGTCGCCGAACTTTGTGAAGATGCTCGGCTACGACAACGCCCCTTCACCGAG 156
                                                                                                                                                      787 CIGGATTAIGGIGCAAATTIIGCICACAIGCIIGGIIICAGIAGCICIGACAIGCAIGAG 846
                                                                                                                                                                                                                 157 CTGATGCGTCTCTATCTGACCATCCACAGTGACCACGAGGGTGGCAACGTGTCTGCCCAC 216
                                                                                                                                                                                                                                                                                                                                             217 ACCGTICACITGGIGGGCICCGCCCICAGCGAICCCIACCITCCITITGCCGCCGGCCIG 276
                                0; Gaps
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On Sep 12, 1996 this sequence version replaced gi:1402331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MO 63108
Pred. No. 4.14e-59;
0; Mismatches 161; Indels
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 472.
Location/Qualifiers
1. .473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
The WashU-HHMI Mouse EST Project
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/organism-"Mus musculus"

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964 TIGAATGGTITAGCIGGACCACTICATGGTITAGCCAATCAGGAACTITIGCTATGGAIC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1024 AAATCTGTTGTAGAGGAGTGTGGGGAAAATTTTCCAAAGAGCAGTTGAAAGACTACGCT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1144 ACTGATCCAAGATACACATGCCAGAGAGTTCGCTTTGAAGCATTTGCCTGAAGATCCA 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 TGGAACACACTCAATTCAGGACGGGTGGTCCA-GGATACGGTCATGCAGTACTGAGGAAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 ACTGACCCTCGCTATTCCTGTCAGCGAGAGTTTGCTCTGAAACATCTGCCTAAAGATCCC 393
                                                                                                                                                                                                                                                                                                                                                                                                                 156 ATGAATGGGCTGGCGGGGCT-CTACATGGACTAGCAAATCAGGAGGTGCTTGTCTGGCTG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 ACACAGCTACAGAAGGAAGTTGGCAAAGACGTGTCAGATGAGAAGTTACGAGACTACATC 274
                                                                                                                                                                                                                                                                                                                                                                                           38 GAGCTCATGCGTTTGTACCTCACCATCCATAGTGACCATGAGGGTGGTAATGTAAGTGC- 96
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                            /clone="IMAGE:889316"
/clone_lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                         Query Match 6.9%; Score 121; DB 14; Length 473; Best Local Similarity 68.2%; Pred. No. 2.08e-58; Matches 264; Conservative 0; Mismatches 119, Indels
                                                                                                                                                                                                                    /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DHIOB"
122 c 124 g 107 t
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                                                                                                                                                                                                                                                                      124 g
/strain-"FVB/N"
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ORIGIN
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US-08-702-718-6.rag

Page 1



Release 3.1A John F. Collins, Biocompusing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 16:59:48 1999; MasPar time 18.52 Seconds 538.628 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from US08702718.pep Description: Perfect Score:

3443 1 MVFYRGVSLLSKLPSPAVQQ ......PLERPKSVTMEWLENHCKKA 469 Sequence.

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11.part11 12:part12 13.part13 13.part14 15:part14 15:part15 16:part16 17:part17 18:part18 19:part14 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part29 30:part30 31:part31 32:part32 33:part38 39:part39

Mean 35.933; Variance 168.408; scale 0.213 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	* Query Match Length DB	DB	ΩI	Description	Pred. No.
1	2443		094	- 1	0.00000		
٠,	0000	200	471	* LC	040704	Dotato citrate synthe	3 550-267
ı m	3098	90.06	471	14	R82838	Potato citrate syntha	3.55e-267
4	2800	81.3	437	14	R82839	Sugar beet citrate sy	7.44e-240
2	313	9.1	436	m	R14357	Citrate synthase enco	1.06e-15
9	116	3.4	456	34	W38570	Methyl tetrahydropter	3.08e+00
7	106	3.1	220	σ	R47340	Fragment of chromaff1	1.47e+01
œ	103	3.0	329	53	W55330	H. pylori ORF hp3e110	2.33e+01
5	103	3.0	329	53	W55574	H. pylori ORF 06ep302	2.33e+01
10	102	3.0	355	24	W29179	Rat ČC chemokine rece	2.71e+01
11	101	2.9	3084	35	W50891	Mouse laminin A chain	3.15e+01
12	98	2.8	355	1	R52749	C-C chemokine recepto	4.95e+01
13	86	2.8	355	24	W25751	Human MIP-lalpha/RANT	4.95e+01
14	96	2.8	355	25	W26588	Human MIP-1 alpha/RAN	4.95e+01
15	95	2.8	2164	~	P81045	Sequence of the viral	7.73e+01
16	95	2.8	2164	Н	P80131	Peptides translated f	7.73e+01

11.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	. ი. പ. დ. പ. ი. დ. დ. დ. დ. പ
SCM525-derived by vaccee potb hor rabidopsis chloralebsiella pneumo cettobacter xylin cettobacter xylin wan placenta G-lymphocyte Tissuman T-lymphocyte Tissuman T-lymphocyte coardia corallin costaglandin-EP3 rostaglandin-EP3 rostaglandin-EP3 uman EP3-V receptalmonella secret	H. pylori secreted or Mature Penicillin V a Soluble type I insuli Full length Penicilli Human CLOCK protein. Sequence of beta-chaicF-5 pathogen resista CF-5 pathogen resista IGF-I receptor.
R85655 R86841 WW60133 WW60133 WW601733 WW73123 R73123 R73123 R73123 R86216 R66216 R66216 R66517 R69513 R69513 R69514 R757810 WY7410	00000000000000000000000000000000000000
23 23 23 25 25 25 25 25 25 25 25 25 25 25 25 25	22 31 31 11 28 4 4 11 11 11 11 11
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## ALIGNMENTS

RESULT 10 R R RESULT 11 R R R RESULT 12 R R R R R R R R R R R R R R R R R R R
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Inhibiting citrate synthase (CS) activity in plants - to inhibit flower formation and improve storage capacity, e.g. in potatoes, a lower formation and anti-scape bold sequences.

Scalaim 5: Page 15-19: 35pp; German.

Claim 5: Page 16-19: 35pp; G
                                                      121 PLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVM 180
                                                                                                                                                                                181 ALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSL 240
                                                                                                                                                                                                                                            241 dyganfahmlgfsssdmhelmklyvtihsdheggnvsahtghlvasalsdpylsfaaaln 300
                                                                                                                                                                                                                                                                                241 DYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGGNVSAHTGHLIHIHIHIHIHIHIHIHIHIH
                                                                                                                                                                                                                                                                                                                                                                   301 glagplhglangevllwiksvveecgeniskeglkdyawktlksgkvvpgfghgvlrktd 360
                                                                                                                                                                                                                                                                                                                                                                                                      361 prytcgrefalkhlpedplfqlvaklyevflgflgnlaklnpwpnvdahsgvllnyyglt 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 plpegllwilltgkvpskeqvdslsgelrsratvpdhvyktidalpvtahpmtqfatgvm 180
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                                                                                                                         181 alqvqsefqkayekgihksklweptyedsmsliaqvplvaayvyrrmykngntipkddsl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Citrate synthase; inhibitor; increased storage capacity; potato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Landschuetze V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 earyytvlfgysralgicsgliwdralglplerpksvtmewlenhckka 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 EARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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Pred. No. 3.55e-267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Landschutze V, Muller-Roeber B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 2
R86383 standard; Protein; 471 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potato citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1994; 408629.
09-MAR-1994; DE-408629
22-SEP-1994; DE-435366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            La Cognata U, Lar
WPI; 95-321536/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T03410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antisense DNA.
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DNA encoding plant citrate synthase - used to regulate flower formation,
                                             120 EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHV-YKTIDALPVTAHPMTQFATG 178
                                                                                       180 vmalqvqsefqkayekgihkskyweptyedsmnliaqvplvaayvyrrmykngdtipkde 239
                                                                                                                    179 VMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRWYKNGNTIPKDD 238
                                                                                                                                                                               240 sldyganfahmlgfsssemhellmrlyvtihsdheggnvsahtghlvasalsdpylsfaa 299
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                                                                                                                                                                                                                                                                                                                    298 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA fragment of citrate synthase from Arabidopsis thallana was firstly amplified using A.thallana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of A. thallana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a CDNA library was prepd. from potato leaves and screened with A. thallana citrate synthase cDNA. Positive clones were purified and sequenced. The nt sequence is given in T04199.
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Disclosure; Page 53-56; 87pp; English.
To identify a cDNA from potato which codes for citrate synthase, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potato citrate synthase.
Citrate synthase; flower formation; tuber storage.
Solanum tuberosum.
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09-MAR-1994; DE-408629.
22-SEP-1994; DE-435366.
19-CCT-1994; DE-438821.
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WPI; 95-328278/42.
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To identify a cDNA from sugar beet which codes for citrate synthase, a cDNA from sugar beet which codes for citrate plaques of this cDNA bank were screened using radioactive DNA probes which comprise a mixture of Solanum tuberosum citrate synthase cDNA (T04199) and Nicotian tabacum citrate synthase cDNA (see T04201). One of the clones was sequenced. The nt. sequence is
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                                                                                                             240 sldyganfahmlgfsssemhellmrlyvtihsdheggnvsahtghlvasalsdpylsfaa 299
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Citrate synthase; flower formation.
Beta vulgaris strain Zuchtlinie 5S 0026
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(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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22-SEP-1994; DE-435366.
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07-MAR-1995; E00859.
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WPI; 95-328278/42.
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Query Match
9.1%; Score 313; DB 3; Length 436;
Best Local Similarity 30.3%; Pred. No. 1.06e-15;
Matches 99; Conservative 87; Mismatches 109; Indels 32; Gaps 28;
                                                       91 eeviylllngelpnkaqydtftntltnhtllheqirnffngfrrdahpmailcgtvgals 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 FAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 vyknfdprakimgqtchevltelgikddplldlavelekials-ddyfvqrklypnvdfy 373
275 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; F1g 5; 12pp; Japanese.

The aarA gene encodes the citrate synthase and is part of an acetic acid resistance operon comprising aarA, aarB and aarC.

The DNA can be used to prepare an acetic acid resistant strain of bacteria for use in acetic acid fermentation.

See also R14358 and 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acetic acid resistant gene with in plasmid and transformed acetobacter - improves yield of acetic acid fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 sqiilkamqiptsmf-tvlfavarttq 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 SGVLLNYYGLTEARYYTVLFGVSRALG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T
R14357 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W38570 standard; Protein; 456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Citrate synthase encoded by aarA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAKA-) NAKANO SUMISE KK.
WPI; 91-329112/45.
                                                                                                                                                                                                                                                                                                                              421 pksvtmewlekfckr 435
                                                                                                                                                                                                                                                                                                                                                                                             454 PKSVIMEWLENHCKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-1991.
05-FEB-1990; 024395.
15-FEB-1989; JP-033776.
05-FEB-1990; JP-024395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetic acid resistance.
Acetobacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AA;
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This sequence represents a Streptococcus methyl tetrahydroptercyltric on homology with an E. coli protein, is a methyl tetrahydroptercyltric glutamate-homocysteine methyltransferase, and is encoded by a DNA of the invention. The DNA sequences were isolated from S. pneumoniae strain of 100093 (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal proposation of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 vrd-vyadlvnlpvdaigl-dfvegkktlelvkggfpadktlyvgivngkniwrnnyeks 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 VPDHVYKTIDALPVTAHPMTQFATGVMALQ-VQSEF--QKAYEKGIHKSK-LWEPTYEDS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 lavlegip-aenivltsscsllh-vpfttaneefepallnhfafavekldeirdl-dair 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 MSLIAQVPLVAAYVYRRMYKNGNTIP-KDDSLDYGANFAHMLGFSSSDMHELMKLYVTIH 268
                                  Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; incculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
Methyl tetrahydropteroyltriglutamate-homocysteine methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fragment of chromaffin granule amine transporter protein. Vesicle membrane transport protein; gene therapy; screening; Parkinsons disease; neurotoxin; identification; detection; antibody; probe; chromaffin granule amine transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vuery Match 3.4%; Score 116; DB 34; Length 456; Best Local Similarity 22.3%; Pred. No. 3.08e+00; Matches 35; Conservative Astones
                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MI, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ngqgsealaank-elfatervgenaelrariagltda 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 SDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Pages 342-344; 483pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R47340 standard; Protein; 220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1994 (first entry)
                                                                                                                                                                                                 pathogenesis.
Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1993,
11-JUN-1993; U05704.
11-JUN-1992; US-899074.
30-JUL-1992; US-923096.
                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1996; US-017670.
                                                                                                                                                                                                                                                                                                                              20-NOV-1997.
14-MAY-1997; U07950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98-008793/01.
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                                                                                                                                                                                                                                                                                        W09743303-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09325699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stodola RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
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Principater pylori nucleic acid sequences and encoded principaters pylori nucleic acid sequences and encoded principaters pylori nucleic acid sequences to treat or prevent H. pylori polypeptide(s) - useful in vaccines to treat or prevent H. pylori claim 14. Pages 556-557: 1145pp. English.

Claim 14. Pages 556-557: 1145pp. English.

Chaim 14. Pages 556-557: 1145pp. English.

Chaim 14. Pages 556-557: 1145pp. English or treat H. pylori polypeptide binding compounds.

Chaim 14. Pages 566-557: 1145pp. English or treat H. pylori life cilon of infection or to identify H. pylori plypeptide binding compounds.

Chaim and probes derived from it may be used for the identification of H. pylori life action. Nucleic complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies can be used to prevent the translation of H. pylori-specific antigens. The genomic sequence of and distribution of H. pylori-specific antigens. The generated complementary shearing the bacterial DNA. The sequences were analysed computer evaluation. To identify 11kely H. pylori antigens for defined by computer evaluation. To identify 11kely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                           New manualian vesicle membrane transport protein - and corresp.

DNA, vectors, transformed cells and antibodies, for diagnosis and transformed cells and antibodies, for diagnosis and transport of neurological disorders, e.g. Parkinson disease

Example 2: Page 114-115; 181pp; English.

The cDNA encoding the chromaffin granule amine transporter protein is useful in gene therapy and as a probe for detecting genomic sequences. The protein is used for screening cytotoxic compounds implicated in Parkinsons disease, diseases associated with activity of neurotoxins or psychiatric disorders and to identify compounds which selectively inhibit or activate its action. Antibodies raised detecting this protein are useful as immunoassay reagents for detecting the protein and as affinity reagents for purfice action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 DSMSLIAQVPLVAAYVYRRMYKNGNT-IPKDDSLDYGANFAHM-LGFSSSD-MHELMKLY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 dnmlltvvvpivptflyatefkdsnsslhrgpsvssqeenvrigilfaskalmqllvnpf 83
                                                                                                                                                                                                                                                                                                                                                                  This fragment of the transporter protein shares homology with the N-terminal domains of the methlenomycin; tetracycline and multi-drug resistance transporter proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1998 (first entry)
H. pylori ORF hp3ell024orf49 protein.
H. pylori oRF hp3ell024orf49 protein.
Gytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1%; Score 106; DB 9; Length 220; 21.1%; Pred. No. 1.47e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 vgpltnrigyhipmfvgfmimf-lstlmfafsgtyallfvartlggigs 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W55330 standard; Protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 21.1%;
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-WAR-1997; U05223.
06-DEC-1996; US-761318.
29-WAR-1996; US-625811.
02-APR-1996; US-758731.
25-CCT-1996; US-738859.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori. W09737044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASTR) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
                    Edwards RH;
WPI: 94-007556/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; V24739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W55330;
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Notice to the protein and the diagnosis of the protein and discretable to treat or prevent H. pylori infection and for diagnosis of H. pylori infection and for diagnosis of H. pylori infection and for diagnosis of H. pylori infection or clear H. pylori sequence is a H. pylori cytoplasmic protein involved in cofactor metabolism. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and acid sequences complementary to the DNA act as antisense sequences and acid sequences complementary to the DNA act as antisense sequences and adistribution of H. pylori minimunoassays to evaluate the abundance and distribution of H. pylori. Specific antigens. The genomic sequence of H. pylori (ATC 5679) was determined from overlapping contigs generated by mechanically shearing the bacternal DNA. The sequences were analysed for SPR of at least 180 nucleotides, and the predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                      membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        24-507-1998 (first entry)
24-507-1998 (first entry)
4. pylori ORF Osep30223_23557202_c2_130 cytoplasmic protein.
Cytoplasmic; vaccine; prevention; freatment; infection; envelope;
identification; binding compound; bacteria; life cycle; activator;
inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
    to other known or exported
                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                   Score 103; DB 29; Length 329; Pred. No. 2.33e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                              8; Indels
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Pred. No. 2.33e+01;
                                                                                                                                                                                                                                                              213 IAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 veempliasvifnrl-kkgmplqmdgalny-qefsh 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 veempliasvifnrl-kkgmplqmdgalny-qefsh 251
                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Mismatches
were analysed for significant homology
                                                                                                                                                                                                                                                                                                                                                                      W55574 standard; Protein; 329 AA.
                                                                                                                                                   Match 3.0%;
Local Similarity 30.6%;
tes 11; Conservative
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Best Local Similarity 30.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1996; US-761318.
29-MAR-1996; US-761318.
20-APR-1996; US-758731.
25-CCT-1996; US-738959.
28-CCT-1996; US-738859.
ASTR A ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
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                                                                                                          329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V24983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9737044-A1.
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                                                                                                            Seguence
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                                                                                                                                                   Query Match
                                                                                        hosts.
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RESULT

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Claim 1: Page 20-21; 26pp; Japanese.
This sequence is a rat CC chemokine receptor. The receptor can be used to screen for novel binding compounds and for preparation of antibodies or antiserum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 lfnlavsdlvflftlpfwidy-klkdnwvfgdamckllsgfyylglyseiffiilltidr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 LFQL-VAKLYEVF-LQFLQNLAKL-NPWPNVDAHSGVLLN-YY-GLTEARYYTVLFGVSR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15, Page 74-79; 132pp; English.

This is the amino acid sequence of the mouse laminin A chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see W50088-99) may include mouse or human laminin A or Al chain, laminin Bl or B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular repeats of the laminin Al chain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC(1998 (first entry)
Mouse laminin A chain.
Laminin, mouse, beta-amyloid; amyloidosis; Alzheimer's disease;
Laminin, mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
Down's syndrome; hereditary cerebral haemornhage; inflammation;
malignancy; Familial Mediterranean Fever; multiple myeloma;
malignancy; Familial Mediterranean Fever; multiple myeloma;
Gertstmann-Straussler syndrome; kuru; scrapie; haemodialysis;
carpal tunnel syndrome; senile cardiac amyloid polymeuropathy;
Familial Amyloidotic Polymeuropathy; thyroid carcinoma; diagnosis;
                                                                                                                                                                                                                                                  CC chemokine receptor protein - useful to screen for novel binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Castillo G, Snow AD;
why: 98-240534(7).
Use of laminin and fragments - for developing products for use in
the diagnosis and treatment of amyloid disease, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2746..2922
//note= "fourth globular domain repeat (Claim 13)"
2690..2700
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.0%; Score 102; DB 24; Length 355; Best Local Similarity 29.5%; Pred. No. 2.71e+01; Matches 26; Conservative 17; Mismatches 38; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "beta-amyloid protein binding region
                                                        Rat CC chemokine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 ylaivhavfslrartvtfgiitsiii-w 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 ALGICSQLIWDRALGLPLERPKSVTMEW 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Claim 12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W50891 standard; Protein; 3084 AA.
W29179 standard; Protein; 355 AA.
                                                                                                                               02-SEP-1997.
22-FBB-1996; 035192.
22-FBB-1996; JP-035192.
(TAKE ) TAKEDA CHEM IND LTD.
WPI; 97-486426/45.
                                    19-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1998.
08-OCT-1997; U18145.
08-OCT-1996; US-027981.
                                                                                                                                                                                                                                                                                                                                                                    355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease or CJD
                                                                                                 rattus.
                                                                                                                                                                                                                                  N-PSDB; T86839
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                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                     and methods can be used for the diagnosis, prognosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary cerebral haemorrhage with amyloidosis of the Dutch type (where the specific amyloid is the beta-amyloid to protein), the amyloidosis associated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid or inflammation association amyloidosis, the amyloidosis associated with multiple myeloma and other B-cell abnormalities (AL amyloid), the amyloidosis associated with prion diseases including Creutzfeldt-dacob diseases, Gertstmann-Straussler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome associated with long-term haemodialysis and carpal tunnel syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1884 selqsragaldrdlen-vrwvslnatsaahvhsniqtlt-eeaewlaa-da-hktanktd 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 lknmtsiyllnlaisdllflftlpfwidy-klkddwvfgdamckilsgfyytglyseiff 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Mismatches 33; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SKLRSRA-VQQTNLSNSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of the C-C chemokine receptor. The sequence can be used in therapeutic or diagnostic compsns. for inflammation and other cytokine mediated disorders. See also R52750-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
the beta-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; 062695.
New C-C chemokine receptor and nucleic acid - are used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prods. for use in diagnosis and therapy of inflammation and other cytokine-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of the thyroid (variant of procalcitonin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polyneuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 35; Length 3084; Pred. No. 3.15e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.95e+01;
15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1940 lise-slas-rqkavlqrssrflkesvqtr 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITVDMVLGGMRGMTGLLWETSLLDPDEGIR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.8%; Score 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-C chemokine receptor.
C-C CKR-1; cytokine; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R52749 standard; Protein; 355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 9; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schall T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 26.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-1995 (first entry)
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ses 22; Conservative
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04-NOV-1993; U10672.
10-NOV-1992; US-974025.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94-183505/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9411504-A.
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Disclosure: Page 15-16; 19pp; Japanese.

This sequence represents human MIP-1 alpha/RANTES receptor (macrophage inflammatory protein 1 alpha/regulated on activation, normal T cell expressed and secreted). The human MIP-1 alpha/RANTES receptor protein may be used in a method for the screening of human MIP-1 alpha/RANTES receptor receptor affinity compounds. The MIP-1 alpha/RANTES receptor coding sequence may be included in an expression vector, preferably pccR, and used to transform a CHO cell for use in the same method. The receptor protein can provide a preventive and treating agent for viral diseases, infectious diseases, tumours, allergy, diabetes, central diseases, hyperlipidaemia, hypercholesterolaemia, osteoporosis, digestive ulcers,
                                                                                                                                                     20-NOV-1997 (first entry)
Human MIP-lalpha/RANTES receptor protein.
Human MIP-1 alpha/RANTES receptor; osteoporosis; pCCR; digestive ulcer;
                                                                                                                                                                                                               macrophage inflammatory protein 1 alpha; diabetes; central disease; regulated on activation, normal T cell expressed and secreted; allergy; affinity compound; expression vector; CHO cell; viral disease; infectious disease; tumour; hyperlipidaemia; hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 lknmtsiyllnlaisdllflftlpfwidy-klkddwvfgdamckilsgfyytglyseiff 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.95e+01;
15; Mismatches 29; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEP-1-sha and RANTES receptor nucleic acid - used to develop products for the detection of these cytokine(s) and their receptors, particularly in inflammatory processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preparation of human MIP-1-alpha/RANTES receptor protein - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human MIP-1 alpha/RANNTES receptor.

Macrophage inflammatory protein-1 alpha; MIP-1 alpha;

reduced upon activation normal T expressed and secreted; RANTES;

receptor; cytokine; antiinflammatory; inflammation; human.

Homo sapiens:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the treatment of viral diseases, tumours, allergy, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24; Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 98;
                                                                                                                W25751 standard; Protein; 355 AA.
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                                                                                                                                                                                                                                                                                                                               08-JUL-1997.
28-DEC-1995; 342130.
28-DEC-1995; JP-342130.
(TAKE) TAKEDA CHEM IND LTD.
WPI; 97-399449/37.
N-PSDB; T86154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 2.8%;
Local Similarity 30.6%;
les 22; Conservative
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28-JAN-1993; 012988.
28-JAN-1993; US-012988.
124 iillitidrylai 135
                                    426 TVLFGVSRALGI 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis etc.
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                                                                                                                                                                                                                                                                                              Homo sapiens.
J09176048-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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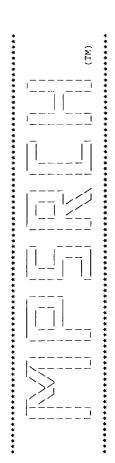
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9
           This polypeptide comprises a claimed receptor for human macrophage inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon a civation normal Texpressed and secreted (RANTES) protein. Also claimed are: a nucleic acid (see T90384) that encodes the receptor: a subsequence of the nucleic acid, having at least 12 contiguous nucleotides; a cell transformed or transfected with the nucleic acid; and purified MIP-1 alpha/RANTES receptor purpoperide. The products can be used for defecting the MIP-1 alpha/RANTES receptor or products can be used for defecting the MIP-1 alpha/RANTES in addition, the receptor can be expressed and used to assay for MIP-1alpha/RANTES in biological samples. The quantitation of MIP-1 alpha/RANTES is biological samples and used to assay for MIP-1alpha/RANTES is biological samples are useful in following the antiinflammatory effects of drugs and prospective usefulness of new antiinflammatory
                                                                                                                                                                                                                                                                                                                                    65 lknmtsiyllnlaisdllflftlpfwidy-klkddwvfgdamckilsgfyytglyseiff 123
                                                                                                                                                                                                                                                                                                                                                                 371 LKHLPEDPLFQL-VAKLYEVF-LQFLQNLAKL-NPWPNVDAHSGVLLN-YY-GLTEARYY 425
                                                                                                                                                                                                                                                                         ' Match
2.8%; Score 98; DB 25; Length 355;
Local Similarity 30.6%; Pred. No. 4.95e+01;
les 22; Conservative 15; Mismatches 29; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of the viral proteins VP1-VP4, P2A-P2C, PCA-P3C encoded by the genomic RNA of rhinovirus strain HRV89 Vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEH) Beehringer Ingelheim.
Duechler M, Skern T, Sommergruber W, Neubauer C, Grundler P, Blaas,
Kuchler E, Frasel L, Zorn M;
Claim 2; Column 15-18; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 15
P81045 standard; Protein; 2164 AA.
P81045;
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/label= P2-A
1008..1101
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/label= P3-A
1497..1517
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/label= PC-2
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70..337
/label= VP2
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/label= VP3
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17-JAN-1987; DE-701301.
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426 TVLFGVSRALGI 437
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                                                                                                                                                                                                                                            355 AA;
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                                                                                                                                                                                                                                              Sequence
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corresponding to viral RNA of rhino-virus HRV89 - useful for

New DNA

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prodn. of polypeptide(s) for stimulating immune system against HRV
                                                                   The viral proteins are used for stimulating a protective immune response and for blocking cellular receptors. Abs against them are useful for assay and purificn. of the corresp. antigen, and can also be used for the therapeutic and diagnostic applications. Sequence 2164 AA;
                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                           Length 2164;
                                                                                                                                                                                                                        Query Match 2.8%; Score 95; DB 2; Length 2164 Best Local Similarity 40.5%; Pred. No. 7.73e+01; Matches 15; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                            1538 vvttdkg-kftglgiydqvmvlpthsdpgseilvdgv 1573
                                                                                                                                                                                                                                                                                                                                                      91 LLDPDEGIRFRGLSIYECOKVLPA-AKPGGEPLPEGL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: Fr1 Oct 22 17:04:01 1999 Job time: 253 secs.
                                                 Claim 8; Fig 4; 66pp; German..
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 17:10:16 1999; MasPar time 7.25 Seconds 758.239 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from USO8702718.pep 3443 I MVFYRGVSLLSKLRSRAVQQ......PLERPKSVIMEWLENHCKKA 469

Description: Perfect Score:

Sequence:

Scoring table:

PAM 150 Gap 11

119857 seqs, 11713122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Database:

Mean 33.542; Variance 164.918; scale 0.203 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ď			SUMMARIES		
Result		Query					
No.	Score	Match	Match Length	DB	ID	Description	Pred. No.
1	106	3.1	220	-	US-08-063-	Sequence 10, Applicati	7.81e+00
2	106	3.1	220	~	PCT-US93-0	10,	7.81e+00
æ	100		361	Н	US-08-415-	37,	1.92e+01
4	86		355	Н	US-08-450-	5, 7	2.58e+01
ß	86	2.8	355	Н	US-08-012-	2,	2.
9	86	٠	355	ĸ	PCT-US95-0	2	2
7	67		624	C 3	US-08-756-	δ	7
80	66	2.7	80	7	US-08-465-	14	5.37e+01
6	93	2.7	80	7	US-09-119-	14,	δ.
10	93	2.7	80	7	US-08-336-	Sequence 14, Applicati	δ.
11	93	2.7	80	-	US-07-971-	14,	η.
12	94	2.7	773	7	US-08-484-	44,	4
13	96	2.7	773	C1	US-08-484-	Sequence 42, Applicati	4.
14	89		253	~	US-08-685-	20,	6
15	89		253	C1	US-09-144-	20,	9.53e+01
16	88		268	7	5320958-6	5	
17	91	5.6	342	Н	US-08-499-	Sequence 5, Applicatio	7
18	91		507	П	US-08-363-	19,	7.16e+01
19	91		532	Н	0	22,	7
20	68		897	Н	us-04-960-	C)	9.
21	68		54	7	US-08-460-	7	9.53e+01
22	89	9.2	1548	C1	US-08-463-	۲,	9.53e+01
23	88		03	Н	-689-LO-SD	5,	1.10e + 02

86 2.5 112 3 PCT-US93-0 Sequence 3, Applicatio 1.46e-4 87 2.5 230 2 US-08-301- Sequence 457, Applicatio 1.46e-4 86 2.5 380 2 US-08-474- Sequence 457, Applicati 1.27e-4 86 2.5 380 2 US-08-474- Sequence 7, Applicati 1.46e-4 85 2.5 380 1 US-08-149- Sequence 7, Applicatio 1.68e-4 85 2.5 380 2 US-08-31- Sequence 7, Applicatio 1.68e-4 85 2.5 436 2 US-08-31- Sequence 7, Applicatio 1.68e-4 85 2.5 436 2 US-08-31- Sequence 7, Applicatio 1.68e-4 85 2.5 500 1 US-08-31- Sequence 3, Applicatio 1.68e-4 85 2.5 500 1 US-08-849- Sequence 7, Applicatio 1.68e-4 85 2.5 500 1 US-08-849- Sequence 7, Applicatio 1.68e-4 85 2.5 500 1 US-08-849- Sequence 2, Applicatio 1.46e-4 86 2.5 879 1 US-08-13- Sequence 2, Applicatio 1.46e-4 86 2.5 879 1 US-08-413- Sequence 2, Applicatio 1.46e-4 87 2.5 1367 2 US-08-413- Sequence 3, Applicatio 1.46e-4 86 2.5 879 1 US-08-413- Sequence 3, Applicatio 1.46e-4 87 2.5 1367 2 US-08-840- Sequence 3, Applicatio 1.46e-4 87 2.5 1367 2 US-08-840- Sequence 2, Applicatio 1.46e-4 87 2.5 1367 2 US-08-840- Sequence 2, Applicatio 1.46e-4 88 2.5 2366 1 US-08-840- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 1 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 86 2.5 2366 2 US-08-405- Sequence 10, Applicatio 1.46e-4 140-4 1	STUDIANOLIA	1 -063-552-10 STANDARD; P	κχχ	Jence 10, Application US/08063552	Sequence 10, Application US/08063552 Patent No. 568836 GENERAL INPORMATION: GENERAL INPORMATION: APPLICANN: Edwards, Robert H TITLE OF INVENTION: Vesicle Membrane Transport Proteins NUMBER OF SEQUENCES: 17 CORRESPONDENCES: 18 COUNTRY: USA ZIP: Pasadena a STREET: 225 South Lake Avenue, Ninth Floor CITY: Pasadena a STREET: 225 South Lake Avenue, Ninth Floor CITY: Pasadena a COUNTRY: USA ZIP: 91101 COMPUTER: READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 18PP C compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/063,552 FILING DATE: 19930514 CLASSIETCATION NUMBER: 32,612 REFERENCE/DOCKET NUMBER	ORIGINAL SOURCE:
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84 VGPLTNRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
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                                                                                                                      208 DSMSLIAQVPLVAAYVYRRMYKNGNT-IPKDDSLDYGANFAHM-LGFSSSD-MHELMKLY 264
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                                                                                              24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 DNMLLTVVVPIVPTFLYATEFKDSNSSLHRGPSVSSQEENVRIGILFASKALMQLLVNPF 83
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9
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TITLE OF INVENTION: Vesicle Membrane Transport Proteins
NUMBER OF SEQUENCES: 17
                                      Ouery Match 3.1%; Score 106; DB 1; Length 220; Best Local Similarity 21.1%; Pred. No. 7.81e+00; Matches 23; Conservative 40; Mismatches 40; Indels
                                                                                                                                                 84 VGPLINRIGYHIPMFVGFMIMF-LSTLMFAFSGTYALLFVARTLQGIGS 131
                                                                                                                                                                        265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 3.1%; Score 106; DB 3; Length 220; Best Local Similarity 21.1%; Pred. No. 7.81e+00; Matches 23; Conservative 40; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05704
                                                                                                                                                                                                                                 220 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sheldon & Mak
225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 795-6321
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: PCT/US93/05704
19930611
                                                                                                                                                                                                                                 PRT;
NISM: Rattus rattus
220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus rattus
ICE 220 AA; 23695 MW; 270630 CN;
                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application PC/TUS9305704
                                                                                                                                                                                                                                                                                                              Sequence 10, Application PC/TUS9305704
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 220 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasadena
California
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HYPOTHERMAN
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                               PCT-US93-05704-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
              SEQUENCE
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ADDRESSE: ADDRESS:
ADDRESSE: PHILLIPS, MOORE, LEMPIO & FINLEY
STRET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: California
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 2.9%; Score 100; DB 1; Length 361; Best Local Similarity 30.0%; Pred. No. 1.92e+01; Matches 15; Conservative 16; Mismatches 17; Indels
265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGL-AG-PLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Positions coded by nonsense codons are NAME/KEY: identified as Xaa.
CE 361 AA; 39600 MW; 808936 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYPEPTIDES BINDING ANTI-
CRYPTOSPORIDIUM ANTIBODIES,
                                                                                                 361 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUFTWARE: DOS
SUFTWARE: METERIE DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAGNOSIS AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Cryptosporidium parvum
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: MAY 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DEFERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: GEECH, JAMES
TITLEON: SUNVENTION: POLYPEPTIDES
TITLE OF INVENTION: CRYPTOSPORIDITILE OF INVENTION: WECTOR AND TITLE OF INVENTION: WECTOR AND TITLE OF INVENTION: WECTOR AND TITLE OF INVENTION: DIAGNOSIS AND WINNERS OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                      Sequence 37, Application US/08415751 Patent No. 5643772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
TELEPAX: (415) 324-1677
TELEPAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                       Sequence 37, Application US/08415751
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                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hana Dolezalova
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                                                                                                                                                                                                                                                                                                               Patent No. 5643772
GENERAL INFORMATION:
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                                                                                                 US-08-415-751-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
     240 SVLLKNGPEFECSYQNVLQDLPQDEMQDLILYNLVDMYWDFLTQNIPIMD 289
              APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
IITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
IITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              Cooley Godward Castro Huddleson & Tatum
                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
CONTRY: USA
ZIP: 9436-215
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 98; DB 1; Length 355;
Pred. No. 2.58e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Mismatches 29; Indels
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                                                      355 AA
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                                                      PRT;
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                                                                                                                      Sequence 5, Application US/08450393A Patent No. 5707815
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CSET, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-843-5165
TELEFAX: 380816COA
                                                                                                     Sequence 5, Application US/08450393A
                                                                                                                                                                                               ADDRESSEE: Cooley Godward C
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: 1:-
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%;
Best Local Similarity 30.6%;
Matches 22; Conservative
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 IILLTIDRYLAI 135
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                                               JT 4
US-08-450-393A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-012-988A-2
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SEQUENCE 355 A
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APPLICANT: Murphy, Philip M.

TITLE OF INVENTION: Cloning and Expression of Human

TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1

TITLE OF INVENTION: alpha)/RANTES Receptor

TITLE OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 LKNMTSIYLLNLAISDLLFLFTLPFWIDY-KLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:: |: |: | :| || :| || 371 LKHLPEDPLFQL-VAKLYEVF-LQFLQNLAKL-NPWPNVDAHSGVLLN-YY-GLTEARYY 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
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GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 98; DB 1; Length 355; Pred. No. 2.58e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
JENCE 355 AA; 41172 MW; 710742 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                  Sequence 2, Application US/08012988A Patent No. 5652133 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application PC/TUS9500476
Sequence 2, Application US/08012988A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.8%;
Best Local Similarity 30.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                       STREET: One Market P
CIIY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Clemente, Thomas E.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Mitsky, Timothy A.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Improved Rhodospirillum Rubrum
TITLE OF INVENTION: POly-B-Hydroxyalkonoate Synthase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; DB 3; Length 355;
Pred. No. 2.58e+01;
15; Mismatches 29; Indels
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRNIT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson STREET: 2010 N. Figueroa Street, 5th Floor CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                          5555-291
                                                                                                                                                                                                                                                                                                                                                                           355 AA; 41172 MW; 710742 CN;
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                                                                                                                                                                        CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BETIANEY, ROBER: 20,121
REGISTRATION NUMBER: 20,121
FELECOMUNICATION INFORMATION:
TELECHONE: 310-977-1001
TELECHAX: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08756317
Patent No. 5849894
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                   Match 2.8%;
Local Similarity 30.6%;
les 22; Conservative
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7TP: 77210-4433
                                                       COUNTRY: USA
ZIP: 90012-2628
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426 TVLFGVSRALGI 437
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                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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90 WIKLLAEQ-PERVIGOOV-SY-WGETLRHFAEAQAAFARGTVTPPPSEGPRDRRFA-NPL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08465273
Patent No. 5866361
GENERAL INFORMATION:
APPLICANT: Choulika, Andre
APPLICANT: Derrin, Arnaud
APPLICANT: Didon, Bernard
APPLICANT: Nicolas, Jean-Francois
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme Patent No. 5866361
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,317
FILING DATE: 25-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/007,693
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,062
REFERENCE/POCKET NUMBER: 33,062
REFERENCE/COCKET NUMBER: 33,062
REFERENCE/COCKET NUMBER: 33,062
RELEPRATION POR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: GAS Aniho acids
                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 97; DB 2; Length 624; 27.1%; Pred. No. 2.99e+01; ative 22; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIF: Z0005-315
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
CE 624 AA; 69538 MW; 1929028 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08465273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 -PEDPLFQLVAKLYEVFLQFLQNLA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1300 I Street, N W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.8%;
Best Local Similarity 27.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Gaps
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APPLICANT: Perrin, Arnaud
APPLICANT: Dujon, Bernard
APPLICANT: Nicolas, Jean-Francois
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
tent No. 5792632
                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.7%; Score 93; DB 2; Length 80;
Best Local Similarity 31.4%; Pred. No. 5.37e+01;
Matches 16, Conservative 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,241
FILING DATE: O7-NOV-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: I-SCEI and the Uses Thereof NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              03495-0111-03000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AA
                                                                           APPLICATION NUMBER: US 07/971,160
FILING DATE: 05-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: POLIEY Jane E. R.
REGISTRATION NUMBER: 33,332
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/336,241
FILING DATE: 07-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/971,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Patent No. 5792632
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           LE TYPE: peptide
80 AA; 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08335241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 03.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1300 I Street, N.W.
                                                                                                                                                                                                                                           TELEPHONE: 202-408-4000
TELEFAX: 202-408-400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                              LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315
COMPUTER READABLE FORM:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunner
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT 10
US-08-336-241-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Patent No. 5948678
GENERAL INFORMATION:
APPLICANT: Choulika, Andre
APPLICANT: Dujon, Bernard
APPLICANT: Dujon, Bernard
APPLICANT: Nicolas, Jean-Francois
IIILE OF INVENTION: Nucleotide Sequence Encoding the Enzyme Patent No. 5948678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 LKSEHG-KVQLGNITVDMV-LG-GMRGMIGLLWETSLLDPDEGIRFRGLSI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIRLMRERDGRNHRDMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93; DB 2; Length 80;
Pred. No. 5.37e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: I-SCEI and the Uses Thereof NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            03495-0111-06000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AA
                                                                                                                                                                                        APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATORNEY/AGENT INFORMATION:
NAME: POLTER, Jane E.R.
PEGISTRATION NUMBER: 33,332
REPERENE/POCKET NUMBER: 03495-0111-TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                        FILING DATE: 07-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,160
FILING DATE: 05-NOV-1992
PRIOR APPLICATION DATA:
             APPLICATION NUMBER: US/08/465,273
FILING DATE: 06-MAY-1995
                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/336,241
FILING DATE: 07-NOV-1994
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 80 AA: 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09119024
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.7%;
Best Local Similarity 31.4%;
Matches 16; Conservative
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20005-3315
                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                             FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-119-024-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
STATE:
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RESULT
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APPLICANT: Plessis, Anne
APPLICANT: Therry, Agnes
TITLE OF INVENTION: I-SCEI and the Uses Thereof
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                            έ,
                                                                                                                                                                                                                         58 LKSEHG-KVQLGNITVDMV-LG-GMRGMIGLLWETSLLDPDEGIRFRGLSI 105
                                                                                                                                                                                                             1 MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIRLMRERDGRNHRDMCV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                           14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENT POUSSING #1.25
SOFTWARE PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/07/971,160
FILING DATE: 19921105
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
                                                                                                                                                                        Query Match 2.7%; Score 93; DB 2; Length 80; Best Local Similarity 31.4%; Pred. No. 5.37e+01; Matches 16; Conservative 14; Mismatches 18; Indels
                                         NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFRENCE/DOCKET NUMBER: 03495-0111-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                    80 AA
              APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/07971160
Patent No. 544896
GENERAL INFORMATION:
APPLICANT: Dujon, Bernard
APPLICANT: Choulist, Andre
APPLICANT: Choulist, Andre
APPLICANT: Fairhead, Cecile
                                                                                                                                                                                                                                                                    PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              MOLECULE TYPE: peptide
JENCE 80 AA; 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/07971160
FILING DATE: 05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                    STANDARD;
       PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3315
COMPUTER READABLE FORM:
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                                                                                                                           amino acid
                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                      TOPOLOGY:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08484101B
Patent No. 5824868
GENERAL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
WORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                          1 MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIRLMRERDGRNHRDMCV
                                                                                                                                                                                                                                                                                Score 93; DB 1; Length 80; Pred. No. 5.37e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/484,1018 FILING DATE: 07-JUN-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
REFERENCE/DOCKET NUMBER: 03495-0111-01000 TELECOMMUNICATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     773
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REPERENCE/DOCKET NUMBER: A-57515-2/RFT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01.5UL-1993
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/08484101B
                                                                                                                                                                                                            MOLECULE TYPE: peptide
JENCE 80 AA; 8936 MW; 32220 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-UUL-1994
                                              TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acids
TYPE: 10FOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 773 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                Query Match 2.7%;
Best Local Similarity 31.4%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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US-08-484-101B-44
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                                                                                                                                                                                                                                    SEQUENCE
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4; Gaps

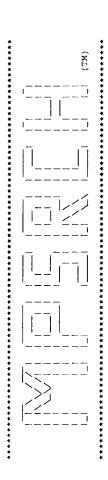
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25; Conservative 28; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXX
          Matches
                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                            115 AKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDAL-PVTAHPMT 173
                                                                                                                                                                                                                          635 AHPHSNSLLRGLQVILVDINDSNRAVTRKLLEKLGCDVIAVSSGFDCLTAIAPGSSSPST 694
                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE OF INVENTION: ETHYLENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7%; Score 94; DB 2; Length 773; 24.0%; Pred. No. 4.64e+01;
                                                                                              Score 94; DB 2; Length 773; Pred. No. 4.64e+01; 28; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                      695 SFQVVVLDLQM-AEMD-GYEVAMRIRSRSWPLIVATTVSLDEEM 736
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   773 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A-57515-2/RFT
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APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-0101-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-011-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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JENCE 773 AA; 85689 MW; 3085314 CN;
MOLECULE TYPE: protein
JENCE 773 AA; 85689 MW; 3085314 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/08484101B Patent No. 5824868 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/08484101B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801 REFERENCE/DOCKET NUMBER: A-1 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           773 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 50
                                                                                                 Query Match 2.7%;
Best Local Similarity 24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3400 Embarca
CITY: San Francisco
STATE: California
                                                                                                                                                                 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Best Local Similarity
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                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                 Matches
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635 AHPHSNSLLRGLQVLLVDINDSNRAVIRKLLEKLGCDVIAVSSGFDCLTAIAPGSSSPST 694
                                            115 AKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDAL-PVTAHPMT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 DYTWNLLKAGKIPEEFNVFNLIQEMRIQRHSAVQTKEQYELVHRAIAQLFEKQLQLY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 DYAWKILKSGKVVPGFG-HGVLR--KTDPRYTCQ-RE-FALKHLPEDPLFQLVAKLY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESSS:
ADDRESSEE: HAMILTON BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 253;
                                                                                        695 SFQVVVLDLQM-AEMD-GYEVAMRIRSRSWPLIVATTVSLDEEM 736
                                                                                                                    APPLICANT: Tonks, Nicholas
APPLICANT: Filmt, Andrew J.
IITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89; DB 2; L
Pred. No. 9.53e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSHL96-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
JENCE 253 AA; 29778 MW; 320375 CN;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08685992 Patent No. 5912138 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08685992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Grandan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHI
TELECHONE: 781.861-6240
TELEPHONE: 781.861-6540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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Best Local Similarity 29.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02173
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                                                                                                                                                                                                   T 14
TS-08-585-992-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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4
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Best Local Similarity 29.8%; Pred. No. 9.53e+01;
Matches 17; Conservative 15; Mismatches 20; Indels 5; Gaps
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BPOOK, SMITH & REYNOLDS, P.C. STREET: Two Millia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows 95
SOFTWARE: FASTEM: Windows 95
SOFTWARE: FASTEM OF WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:
PRIOR APPLICATION:
APPLICATION:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                             Sequence 20, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
              253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 253 AA; 29778 MW; 320375 CN;
                                                                                        Sequence 20, Application US/09144925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
              STANDARD;
                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: USA
ZIP: 02421-4799
LT 15
US-09-144-925-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                        XXXXXX
  RESULT
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Search completed: Fri Oct 22 17:10:33 1999 Job time : 17 secs.

Page



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 22 17:04:20 1999; MasPar time 20.94 Seconds 897.479 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from US08702718.pep 3443

Description: Perfect Score:

1 MVFYRGVSLLSKLRSRAVQQ.....PLERPKSVTMEWLENHCKKA 469 Sequence:

Scoring table:

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 50.451; Variance 107.716; scale 0.468 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## DOTT OF A STATE OF

	Description Pred. No.	ethanolamine ammonia- 0.00e+00	probable citrate (si) 0.00e+00	(si)-synthase 0.	)-synthase 0.	-synthase 0.	_	H	-synthase 1.	nt protei 1.	9	ς.	4	ISe 1.	6	gltA 6	(si)-synthase 1		(si)-synthase		synthase (cit 3.79	- cu 5.5	citrate synthase . He 2.60e-23	citrate synthase II ( 3.65e-21
ES	Description	ethanolami		$\sim$	3	S	s)	S	$\sim$	14-nm fila	~	_	01				-	-	citrate (s	probable g	rn.			itrate
SUMMARIES	ID	S44316	T02390	YKMUM	YKPG	S42370	YKBY	YKBYC	S41563	JC5625	S52814	140717	A43936	YKQPC	E69658	S74344	139506	YKFSCA	JQ1392	E70782	C69417	S53007	D71982	009690
	DB	7	C4	П	Н	C1	П	Н	7	C1	7	7	7	٦	7	C1	C1	_	c a	7	7	C1	(1	C3
	Length	471	474	472	464	458	479	460	469	462	486	437	373	436	372	397	424	4.28	430	431	372	$\vdash$	426	372
æ	Query	90.0		71.3	٠.		51.2			40.2		10.5		9.0		8.9							٠.	7.2
	Score	3098	2987	2454	02	1820	1763	1679	1680	1385	1218	360	347	310	305	306	287	285	274	275	272	271	192	248
	Result No.	-	Ci	٣	4	2	9	7	8	60	10	11	12	13	14	15	16	17	18	19	20	Çį	C4	23

360 KIVPRYTCOREFAMKHLPEDPLFOLVSKLYEVFLLFLONLAKLKPWPNVDAHSGVLLNYY 419

300 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLR 359

QQ 0.7 ď

1.13e-20 3.09e-18 2.85e-17 8.59e-18 8.59e-17 2.07e-12 2.07e-12 2.07e-12 3.59e-01 3.88e-00 3.00e+00 3.88e-00 3.88e-00 3.88e-00 3.88e-00 3.88e-00 3.88e-00 3.88e-00 3.88e-00 3.88e-00	ange 3.	Gaps 4: KKIK 60   :     :     :   KFGG 119       KPGG 119      KPG 119      KPG 119      KPG 119      KPG 119      KPG 119     KPG 119      KPG 119      KPG 119      KPG 119      KPG 119      KPG 119      KPG 119      KPG 239       KPG 239
citrate synthase - He citrate (si) synthase citrate synthase I (c citrate synthase probable citrate synthase protein translocas BCK2 protein - yeast DNA topoisomerase (AT amhodeoxychorismate hypotherical protein macrophage inflammato cell division protein fts 2 protein - Strept RNA-directed DNA polydynactin - mouse dynein-associated pro	se (EC 4.3.1.7) - potato erosum #common_name potato vision 10.Nov-1995 #text_chang tzer, L.; Mueller-Roeber, B. ta Library, September 1993 :9483509; PID:9483510 )-synthase trogen lyase weight \$2612 #checksum 4730	DB 2; Length 471; ches 22; Indels 4; ches 22; Indels 4; SSGLDLRSELVQELIPEQODRLK SSGLDLRSELVQELIPEQODRLK SSGLDLRSELVQELIPEQODRLK SSGLDLRSELVQELIPEQODRLK SSGLDLRSELVQELIPEQODRLK SSGLDLRSELVQELIPEQODRLK SSGLDLRSELVQELIPEQORLE SSGLDLRSELVQENTHINIII SSGLDLRSELVGRYCHPAAK SPHY-YKTIDALPVTAHPWTOF SSGLVAAYVYRRMYKNGDTIP INQVPLVAAYVYRRMYKNGDTIP INQVPLVAAYVYRRMYKNGDTIP SGGNVSAHTGHLVASALSDPYLS EGGNVSAHTGHLVASALSDPYLS EGGNVSAHTGHLVASALSDPYLS
2 KKEC 2 KKEC 2 140044 2 140044 2 140044 2 140080 2 140380 2 140380 2 140380 2 140380 2 140380 3 150380 3 150380	ALIGNMENT  ALIGNMENT  ammonia-lya  Solamum tub  isequence_re  reguence_re  v.; Willmi  the EMBL Da  the EMBL	90.0%; Score 3098; 89.6%; Pred. No. 0.0 vative 23; Mismatci SRAVQSNVSNVSNVRULOVQTS
10.00	440.0444044 DIES	90.0%; S Conservative 2 Conservative 2 SLLSKLRSRAVQSNVS SLLSKLRSRAVQCNVS SLLSKLRSRAVQCNVIS SLLSTLIN
222234 44.022344 44.02234 10041111114 100414 100114	1 S4 S4 S5	S S S S S S S S S S S S S S S S S S S
40000000000000000000000000000000000000	RESULT ENTRY TITLE ORGANISM DATE ORGENISM ACCESSION REFERENCE #AUTHO # # # CLASSIFIC KEYMORDS SUMMARY SUMMARY	Ouery Best Lamatche Db Oy 6 0y 6 0y 6 0y 12 0y 12 0y 17 0y 17 0y 17 0y 17 0y 17 0y 17 0y 23

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carbon-carbon lyase; oxo-acid-lyase; tricarboxylic acid cycle
#length 474 #molecular-weight 52782 #checksum 6960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, May 1998
Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
                      417
                                                                                                                                                                                                                                       probable citrate (si)-synthase (EC 4.1.3.7) - Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17/3; 39/3; 53/3; 75/3; 97/3; 135/3; 157/1; 184/3; 201/2; 22//2; 270/2; 284/3; 313/3; 347/3; 383/3; 400/3; 425/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SEHGKVOLGNITVDMVIGGMPGMTGLLWETSLLDPEEGIPFPGLSIPECQKVLPTAQSSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 SEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 EPLPEGLIWLLIGKVPSKEQVEALSKDLANRAAVPDYVYNAIDALPSTAHPMTQFASGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 MALQVQSEFQKAYENGIHKSKFWEPTYEDCLNLIARVPVVAAYVYRRMYKNGDSIPSDKS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDYGANFSHMLGFDDEKVKELMRLYITIHSDHEGGNVSAHTGHLVGSALSDPYLSFAAAL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 LDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAAL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYCHGVLRNT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGLAGPLHGLANQEVLLWIKSVVEECGENISKEOLKDYAWKTLKSGKVVPGFGHGVLRKT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPRYVCOREFALKHLPDDPLFQLVSKLYEVVPPVLTELGKVKNPWPNVDAHSGVLLNHYG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPRYTCOREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKL-NPWPNVDAHSGVLLNYYG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKSQLQELIPEQQDRLKKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVFYRGVSLLSKLRSRA-VQQTNLSNSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLK 59
                                                                                                                                                                                                                                                                                                              #formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                                                           05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 KTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
2;
                                                                                               418 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTWEWLENHCKKA 469
                                                                    420 GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:AC004521; NID:g3128166; PID:g3128180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 0.00e+00;
53; Mismatches 27;
                                                                                                                                                                                                                 *type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-474 ##label ROU
                                                                                                                                                                                                                                                                                       F4I1.16 protein
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es 389; Conservative
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                                                                                                                                                                                                                                                                 thaliana
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citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *#cross-references EMBL:X17528; NID:g11243; PID:e1188578; FID:g2652924
*#note the sequence from Fig. 2 is inconsistent with that from
Fig. 1 in having 47-Gly, 125-Trp, 141-Leu, 151-Ser,
185-Asn, 187-Asn, 191-Asn, 348-Leu, an additional Gly
after 89-Trp, an additional Val after 393-Cys and two
additional Arg after 228-Arg, in lacking 114-Leu and
residues 333 to 241
                                                                                                                                                                                                                                                                                                                                           #Journal Plant Mol. Biol. (1989) 13:411-418
#title isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana.
#cross-references MUID:91370823
                                                                                                                                                                                                                                                                                                                    Unger, E.A.; Hand, J.M.; Cashmore, A.R.; Vasconcelos, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SEHGKVOLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQK-VLPAAKPG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 G-EPLPEGLL-WLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMT0FA 176
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                                                                                                                                                                         #formal_name Arabidopsis thaliana #common_name mouse-ear
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#length 472 #molecular-weight 52941 #checksum 9626
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oxo-acid-lyase; tricarboxylic acid cycle
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                                                                                                                                                                                                                                 #authors Evans, C.T.; Owens, D.D.; Sumegi, B.; Kispal, G.; Srere, P.A.
#journal Biochemistry (1988) 27:4680-4686
#title Isolation, nucleotide sequence, and expression of a cDNA
encoding pig citrate synthase.
#cross-references MUID:89000665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ts annotation: X-ray crystallography, 2.7 and 1.7 angstroms Cirrate (si)-synthase is found in nearly all cells capable of cidative metabolism. It catalyzes the condensation of oxaloacetate and acetyl-CoA to form citrate in the tricarboxylic
                                                                                 YRPG #type complete cirate (si)-synthase (EC 41.3.7) precursor - pig formal name Sus scrota domestica #common_name domestic pig 15-oct-1982 #sequence_revision 30-Sep-1992 #text_change
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#modified_site N6,N6-trimethyllysine (Lys) #status
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Complete amino acid sequence of porcine heart citrate
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*journal J. Mol. Biol. (1982) 158:111-152

*title Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7

*cross-references MUID:83010291
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417 YGLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
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#accession A01109
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27 SASSINLKDILADLIPKEOARIKTFROOHGNIVVGOITVDMMYGGMRGMKGLVYEISVLD 86

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S42370 #type complete citrate (si)-synthase (EC 4.1.3.7) precursor - Caenorhabditis
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                                                                                                        87 PDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAA 146
                                                                                                                                                                                                                                                                                                                     154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI 213
                                                                                                                                                                                                                                                                                                                                                                                            207 AKLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 KLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCOREFALKHLPHDPMFKLVAQLYKIVPN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 ARADLPTHVVRMLDNFPDNLHPMAQFIAAIAALNNESKFAGAYARGVAKASYWEYAYEDS 204
                                                                                                                                                                           94 PDEGIPFPGLSIYECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELPSPAT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AQVPLVAAYVYRRMYKNGNTI-PKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 GGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 GGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 QLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 FLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIWDRALGLPL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 SVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWN 144
34 ISSGLDLRSELQELIPPQQDRLKKLKSEHGKVQLGNIIVDMVLGGMRGMTGLLWETSLLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 LSTSAEGSTNLKEVLSKKIPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTET 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 LQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWET 89
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07-0ct-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                              147 LPSHVVTMLDNFPINLHPMSQLSAAITALNSESNFARAYAEGIHRIKYWELIYEDCMDLI
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carbon-carbon lyase; mitochondrion; oxo-acid-lyase
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Best Local Similarity 56.5%; Pred. No. 0.
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EMBO J. (1984) 3:1773-1781
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening
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Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
submitted to the EMBL Data Library, January 1994
Twelve open reading frames revealed on the 23.6 kbp segment
flanking the centromere on the Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                            YKBY *type complete citrate (si)-synthase (EC 41.3.7) precursor, mitochondrial yeast (Saccharomyces cerevisiae) protein N2019; protein YNR001c
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##note the nucleotide sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae
                                                                                                                                                                                                               389 VFLQFLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGIC-SCLIWDRA 446
                        269 SDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLHIKSVVEECGEN 328
                                                                                                                       329 ISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYE 388
                                                                                                                                                                                        385 ITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARG 443
                                                                                            325 YTEEQLKEWVWKHLKSGQVVPCYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSTLYK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #formal_name Saccharomyces cerevisiae
25-Feb-1985 #sequence_revision 10-Feb-1995 #text_change
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265 SDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFN
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Yeast (1994) 10:1355-1361
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S35390; S45124; S48338; A01110; S63327
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##residues 1-479 ##label LIN
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**residues 1-479 **label VER
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##cross-references EMBL:271616; NID:g1302468; PID:e239778; PID:g1302469; MIPS:YNR001c
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                                                                                                                                                                                                                                                                                                                            carbon-carbon lyase; catalyzes condensation of oxaloacetate and acetyl-CoA to form citrate; oxo-acid-lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 PDEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRAT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDHEG 278
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predicted #label TNP\
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#length 479 #molecular-weight 53360 #checksum 4
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                                                                                                                                                                                                  ##cross-references SGD:S0005284; MIPS:YNR001c
                                                                                                                           ##experimental_source strain S288C
                       **#molecule_type DNA
**residues 1-479 **label AER
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                                           P.A.; Guarente, L.P.
Mol. Cell. Biol. (1986) 6:4509-4515
Mitochondrial and nonmitochondrial citrate synthases in
Saccharomyces cerevisiae are encoded by distinct homologous
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                                                                                                                                                                                                                                                                                                                   Biteau, N.; Fremaux, C.; Hebrard, S.; Menara, A.; Aigle, M.;
                                                                                                                                                                                                                                                                                                                                                          Yeast (1992) 8:61-70
The complete sequence of a 10.8kb fragment to the right of
the chromosome III centromere of Saccharomyces cerevisiae.
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acetyl-CoA; carbon-carbon lyase; homodimer; oxo-acid-lyase;
peroxisome; tricarboxylic acid cycle
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#active_site His, His, Asp #status predicted
#length 460 #molecular-weight 51413 #checksum 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 SADIMSRSELPSHVVQLLDNLPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSY 190
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                     Rosenkrantz, M.; Alam, T.; Kim, K.S.; Clark, B.J.; Srere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liao, X.; Small, W.C.; Srere, P.A.; Butow, P.A. Mol. Cell. Biol. (1991) 11:38-46
Intramitochondrial functions regulate nommitochondrial citrate synthase (CII2) expression in Saccharomycos
                                                                                                                                                                                                                                                ##cross-references EMBL:211113; NID:93297; PID.93299; GB:M14685; NID:9171227
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*accession S26734
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#cross-references MUID:87089811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Gen. Genet. (1994) 242:105-110
Characterization of the cit-1 gene from Neurospora crassa
encoding the mitochondrial form of citrate synthase.
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                                                                                                                                                                                   311 VNDDYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHFPDYELFKLVS 370
                                                                                                                                                                                                                                                                                                            371 SIYEVAPGVLTEHGKTKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQLIT 430
                                                                                                                                                                                                                                                                                                                                            385 KLYEVFLQFLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSQLIW 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 TIAARIYQNVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELLRLYLTIHTDHEGGNV 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 YAWKTLKSGKVVPGFGHGVLRKTDPRYTCOREFALKHLPEDPLFOLVAKLYEVFLOFLOF
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                                                                                                                                                                                                                       325 CGENISKEQLKDYAWKILKSGKVVPGFGHGVLRKIDPRYICQREFALKHLPEDPLFQLVA 384
205 TYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLY 264
                                                                                                                     265 VIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 LPSELQELIPEQODPLKKLKSEHG-KVQLGNITVDMVLGGMRGMIGLLWETSLLDPDEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 LKERFAELLPENIEKIKALRKEHGSKV-VDKVTLDQVYGGARGIKCLVWEGSVLDAEEGI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Neurospora crassa
20-May-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36/3; 58/2; 123/1; 453/2
superfamily citrate (si) synthase
earbon-carbon lyase; mitochondrion; oxo-acid-lyase
#length 469 #molecular-weight 52002 #checksum 490
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48.8%; Score 1680; DB 2, I
Best Local Similarity 56.2%; Pred. No. 1.00e-293;
Matches 244; Conscrvative 78; Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 DRALGLPLERPKSVTME 460
                                                                                                                                                                                                                                                                                                                                                                                                                                    431 DRAIGASIERPKSYSTE 447
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#title
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Numata, O.; Takemasa, T.; Takagi, I.; Hirono, M.; Hirano, H.; Chiba, J.; Watanabe, Y.
Biochem. Biophys. Res. Commun. (1991) 174:1028-1034
Tetrahymena 14-nm filament-forming protein has citrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain transit peptide (mitochondrion) *status
predicted *label TNP\
*product 14-nm filament protein/citrate synthase *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     **residues 1.462 **label NUM

**cross-references GB:D90117; NID-9217406; PID:d1014848; PID:g1588046

**note part of this sequence, including the amino end of the mature protein, was confirmed by protein sequencing mature protein, oral morphogenesis preceding binary fission, and in nuclear events during fertilization, such as formation of gametic pronuclei and zygote formation of gametic pronuclei and intochondrial enzyme, citrate
84 IIFRCYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQNR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 IRFRGLSTYECOKVLP-A-AKPG--G--EPLPEGLLWLLTGKVPSKEQVDSLSGELPSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 GTVNQDCVNF1LNLPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYEDSM 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 ATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKG-IHKSKLWEPTYEDSM 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 DLIAKIPRVAAIIYRHKYRDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECIRGYLSIHCD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 NLKKVIAEIIPQKQAELKEVKEKYGDKV-VGQYTVKQVIGGMRGMKGLMSDLSRCDPYQG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 DLRSELQELIPEQODRLKKLKSEHG-KVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEG 97
                                                                                                                                                                                                                                                                14-nm filament protein/citrate synthase (EC 4.1.3.-) -
Tetrahymena thermophila (SGC5)
49K filament-forming protein
#formal_name Tetrahymena thermophila
14-0ct.1997 #sequence_revision 07-Nov-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. (1997) 237:205-210
Direct demonstration of the bifunctional property of
Tetrahymena 14-nm filament protein/citrate synthase
following expression of the gene in Escherichia coli
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oxo-acid-lyase
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Local Similarity 49.0%; Pred. No. 1.29e-235;
Nes 215; Conservative 89; Mismatches 123;
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                                                                              456 SYSTDKWIEI-CKK 468
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**cross-references EMBL:U31900; NID:g1276597; PID:g939735; MIPS:YPR001w
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##experimental_source strain AB972
**NCE S57724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.;
Hall, J.; Storms, R.K.; Vo, D.H.; Winnett, E.
Submitted to the EMBL Data Library, July 1995
The sequence of Saccharomyces cerevisiae chromosome XVI righ
                                                                                                                      271 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 330
                                                                                                                                                                                                                                                                                                391 LQFLQNLAKL-NPWPNVDAHSGVLLNYGLTEARYYTVLFGVSRALGIC-SQLIWDRALG 448
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                         211 SLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSD 270
                                                                        264 HEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTKVS 323
                                                                                                                                                                       324 DKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCADVI 383
                                                                                                                                                                                                                                                                      384 PKKLLTYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSRAFG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          citrate (si)-synthase (EC 4.1.3.7) - yeast (Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Saccharomyces cerevisiae
19-May-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jia, Y.K.; Becam, A.M.; Slonimski, P.P.; Herbert, C.J.
submitted to the EMBL Data Library, June 1995
S57724
                                                                                                                                                                                                   32 VQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSL
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#length 486 #molecular-weight 53811 #checksum 9998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein LPZ1w; protein YP9723.01; protein YPR001w
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852814
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35.4%; Score 1218; DB 2; L
Best Local Similarity 45.0%; Pred. No. 6.61e-203;
Matches 205; Conservative 102; Mismatches 124;
##cross-references SGD:S0006205; MIPS:YPR001w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *type complete
Pearson, D.; Bowman, S.
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##residues 1-486 ##label JIA
                                                                                                                                                                                                                                                                                                                                                                     443 LPIERPGSADLKWFHDKYR 461
                                                                                                                                                                                                                                                                                                                                                                                                                   449 LPLERPKSVIMEWLENHCK 467
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14   PGFKLPHYTEKVLSSLPKDMHPMTOLAIGLASMNKGSLFATNYQKGLIGKMEFWKDTLED 200	321 EVVRFLIEMNSNIS-STAREQEIKDYLWKILNSNRVIPGYGHAVLRKDDRRFTAMLEFAQ 379   : : : :     :	NULT 11 #type complete  LE citrate (si)-synthase (EC 4.1.3.7) - Corynebacterium glutamicum #formal_name Corynebacterium glutamicum 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 17-Jul-1998 140717 ESSIONS 140717 ELManns, B.J.; Thum-Schmitz, N.; Eggeling, L.; Luedtke, K.U.; Sahm, H. #journal Microbiology (1994) 140:1817-1828 #title of the Corynebacterium glutamicum gltA gene encoding citrate synthase.	Istatus preliminary; translated session 1407 ##label RES residues 1-437 ##label RES offices references EMBL: X66112; NID: 9505; and properties offices references EMBL: X66112; NID: 9505; and properties offices offi	#active_site His #status predicted  #length 437 #molecular-weight 48929 #checksum 2093  y Match  Local Similarity 30.4%: Pred. No. 2.58e-40;  hes 96; Conservative 89; Mismatches 105; Indels 26; Gaps 22;  97 LLINGELPTPDELHKFNDEIRHH-TLLDEDFKSQFNVFPRDAHPMATLASSVNILST-Y- 153
Db 141 Oy 151 Db 201 Oy 205 Db 261 Oy 256		RESULT 11 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE # authors # journal # title	######################################	10 6 6 6

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#authors Schendel, F.J.; August, P.R.; Anderson, C.R.; Hanson, R.S.;
Flickinger, M.C.
#journal Appl. Environ. Microbiol. (1992) 58:335-345
#title Cloning and nucleotide sequence of the gene coding for citrate synthase from a thermotolerant Bacillus sp.
#cross-references MUID:92171501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##note sequence inconsistent with the nucleotide translation sequence extracted from NOBI backbone (NCBIP:84047)

CLASSIFICATION #superfamily citrate (si)-synthase summARY #length 373 #nolecular-weight 41970 #checksum 2911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 MITGKKPTELEEKIFDRSLVLYSEHELPN-STFTARVIASTLSDLYGALTGAVASLKGHL 222
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10.1%; Score 347; DB 2; Length 373;
Best Local Similarity 30.3%; Pred. No. 4.98e-38;
Matches 96; Conservative 80; Mismatches 117; Indels 24; Gaps
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*formal_name Bacillus sp.
10-Mar-1993 *sequence_revision 18-Nov-1994 *text_change
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##molecule_type nucleic acid; protein
##residues 1-373 ##label SCH
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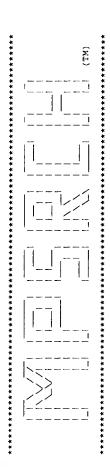
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Alloni, G.; Azevedo, V.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Cadwell, B.; Capuano, V.; Curnter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Curmings, N.J.;
Daniel, R. A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujtta,
M.; Fujtta, Y.; Funa, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             carbon-carbon lyase; oxo-acid-lyase; catalyzes synthesis of citrate from acetyl-CoA and oxaloacetic acid tricarboxylic acid cycle
                                                                                                                                                                       Cloning of genes responsible for acetic acid resistance in Acetobacter aceti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 EGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%; Score 310; DB 1; Length 436;
00.3%; Pred. No. 1.33e-31;
ttive 87; Mismatches 109; Indels 32; Gaps
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allosteric regulation; carbon-carbon lyase; homohexamer;
oxo-acid-lyase; tricarboxylic acid cycle
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 436 #molecular-weight 48196 #checksum 9071
                                                                                     Fukaya, M.; Takemura, H.; Okumura, H.; Kawamura, Y.;
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                                                                                                                                                                                                                                                                                         *#molecule_type DNA
*#residues 1-436 ##label FUK
##cross-references GB.M34830, NID.9141729; PID:9141730
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                                                                                                                 Horinouchi, S.; Beppu, T.
J. Bacteriol. (1990) 172:2096-2104
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Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holasppel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A., Lardinois, S.; Luuber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maudel, C.; Medique, C.; Medida, N.; Mellado, R.P.; Mizuno, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott, A.M.; Posteren, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Roche, B.; Rosse, M.; Sadaie, Y.; Stro, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sckowska, A.; Serro, R.; Scroft, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Taraconi, E.; Takadi, T.; Takahashi, H.; Tarkemaru, K.; Takeuchi, M.; Tamakoshi, A.; Taranka, T.; Terpstra, P.; Togoni, A.; Tasarotti, A.; Vanane, K.; Vasumoto, W.; Vatati, A.; Vasta, K.; Yasumoto, W.; Vatati, R.; Yasumoto, W.; Vatata, K.; Yoshida, A.; Yanane, K.; Yasumoto, W.; Vatata, K.; Yoshida, A.; Tamaka, H.F.; Zumstein, E.; Vechikada, H.; Parane, P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99; Mismatches 118; Indels 27; Gaps 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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##cross-references GB:Z99116; GB:AL009126, NID:g2634723; PID.e1185682;
PID:g2634848
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Best Local Similarity 27.8%; Pred. No. 9.59e-31;
Matches 94; Conservative 99; Mismatches 118
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Nature (1997) 390:249-256
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##molecute_type DNA
##residues 1-397 ##label KAN
##cross-references EMBL:064001; GB:AB001339; NID:g1001102; PID:d1010913;
PID:g1001122
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
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                                                                                                                                                                                                                                                                                     #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamcto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Marki, A.; Nakazaki, N.; Natuo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Natuo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.; Minpo, S.; Takeuchi, S.; Minpo, S.; Takeuchi, S.; Minpo, S.; Takeuchi, S.; Minpo, S.; Takeuchi, S.; Minpo, P.; Minpo, P.; Minpo, S.; Minpo, Minpo, S.; M
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                                                                                PCC 6803
25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
21-Aug-1998
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8.9%; Score 306; DB 2; Length 397;
Best Local Similarity 30.8%; Pred. No. 6.46e-31;
Matches 97; Conservative 76; Mismatches 112; Indels
hypothetical protein s110401
#formal_name Synechocystis sp.
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CLASSIFICATION
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    ALTERNATE_NAMES
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protein - protein database search, using Smith-Waterman algorithm

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PAM 150

Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 51.766; Variance 94.679; scale 0.547

## SUMMARIES

Length DB ID Description  471   CISY_CRITMA CITRATE SYNTHASE, MITO 0. 472   CISY_CREAT CITRATE SYNTHASE, MITO 0. 644   CISY_CREAT CITRATE SYNTHASE, MITO 0. 648   CISY_CAREL CITRATE SYNTHASE, MITO 0. 648   CISY_CAREL CITRATE SYNTHASE, MITO 0. 647   CISY_CANTR CITRATE SYNTHASE, MITO 0. 647   CISY_CANTR CITRATE SYNTHASE, MITO 0. 647   CISY_CANTR CITRATE SYNTHASE, MITO 0. 645   CISY_CANTR CITRATE SYNTHASE (EC 4 4. 673   CISY_CANTR CITRATE SYNTHASE (EC 4 5. 674   CISY_CANTR CITRATE SYNTHASE (EC 4 4. 678   CISY_CANTR CITRATE SYNTHASE (EC 4 4	;		æ						
2932 85.2 471 1 CISY_CITMA CITRATE SYNTHASE, MITO 2015 2021 85.2 471 1 CISY_CARATH CITRATE SYNTHASE, MITO 2016 2021 86.3 436 1 CISY_CHICK CITRATE SYNTHASE, MITO 0.1944 56.5 433 1 CISY_CHICK CITRATE SYNTHASE, MITO 0.195 51.8 482 1 CISY_CAREL PROBABLE CITRATE SYNTH 0.1740 50.5 467 1 CISY_CART CITRATE SYNTHASE, MITO 0.1740 50.5 467 1 CISY_CART CITRATE SYNTHASE, MITO 0.1744 49.8 475 1 CISY_CART CITRATE SYNTHASE, MITO 0.1744 49.8 469 1 CISY_CART CITRATE SYNTHASE (EC 4 4.174 6.174 4.174 6.174 4.174 6.174 4.174 6.174 4.174 6.174 4.174 6.174 4.174 6.174	. 1	Score	Query		DB	ID	Description		
2454 71.3 472 1 CISY_ARATH CITRATE SYNTHASE, MITO 0. 1924 58.7 464 1 CISY_EDG CITRATE SYNTHASE, MITO 0. 1924 55.5 438 1 CISY_CHICK CITRATE SYNTHASE, MITO 0. 1929 52.9 468 1 CISY_CAEEL PROBABLE CITRATE SYNTH 0. 1763 51.8 482 1 CISY_CAEL PROBABLE CITRATE SYNTH 0. 1740 50.5 467 1 CISY_CAENT CITRATE SYNTHASE, MITO 0. 1740 50.5 467 1 CISY_CAENT CITRATE SYNTHASE, MITO 0. 1744 49.8 475 1 CISY_CAENT CITRATE SYNTHASE, MITO 0. 1679 48.8 469 1 CISY_ASPNG CITRATE SYNTHASE, MITO 0. 1885 40.2 46.9 1 CISY_ASPNG CITRATE SYNTHASE, MITO 0. 1885 40.2 46.9 1 CISY_ASPNG CITRATE SYNTHASE, MITO 0. 1885 40.2 46.9 1 CISY_TEAST CITRATE SYNTHASE, MITO 0. 1885 40.2 486 1 CISY_TEAST CITRATE SYNTHASE, MITO 0. 1885 40.3 1 CISY_TEAST CITRATE SYNTHASE (EC 4 4. 310 373 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 380 372 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 380 372 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 372 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 372 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 372 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 5. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 4. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 4. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 4. 381 382 423 1 CISY_BACC CITRATE SYNTHASE (EC 4 4. 381 381 381 381 381 381 381 381 381 381	_	2932	85.2	471	-	CISY_CITMA		MITO	0.00e+00
2021 58.7 464 1 CISY_PIG CITRATE SYNTHASE, MITO 0 1944 56.5 433 1 CISY_CAELEL PROBABLE CITRATE SYNTHO 0 1984 56.5 483 1 CISY_CAELEL PROBABLE CITRATE SYNTH 0 1782 51.8 482 1 CISY_CAELEL PROBABLE CITRATE SYNTH 0 1740 50.5 467 1 CISY_CANTR CITRATE SYNTHASE, MITO 0 1740 50.1 474 1 CISY_CANTR CITRATE SYNTHASE, MITO 0 1750 488 460 1 CISY_CANTR CITRATE SYNTHASE, MITO 0 1767 48.8 460 1 CISY_CANTR CITRATE SYNTHASE, MITO 0 1767 48.8 460 1 CISY_CAELT CITRATE SYNTHASE, MITO 0 1768 48.8 460 1 CISY_CAELT CITRATE SYNTHASE, MITO 0 1768 48.8 460 1 CISY_CAELT CITRATE SYNTHASE, MITO 0 1768 48.8 460 1 CISY_CAELT CITRATE SYNTHASE, MITO 0 1769 48.8 460 1 CISY_CAELT CITRATE SYNTHASE, MITO 0 1769 48.8 460 1 CISY_CAELT CITRATE SYNTHASE, MITO 1 1769 48.8 460 1 CISY_CAELT CITRATE SYNTHASE, MITO 1 1769 48.8 460 1 CISY_CAELT CITRATE SYNTHASE (BC 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	~	2454	71.3	472	٦	CISY_ARATH		MITO	0.00e+00
1944   56.5   433   1   CISY_CHICK   CITRATE SYNTHASE, MITO   1820   52.9   468   I CISY_CAREL   PROBABLE CITRATE SYNTH   0. 1763   51.2   479   I CISY_SCHPO   PROBABLE CITRATE SYNTH   0. 1725   50.1   479   I CISY_CANTR   CITRATE SYNTHASE, MITO   0. 1725   50.1   474   I CISY_EAST   CITRATE SYNTHASE, MITO   0. 1714   49.8   475   I CISY_EMBNI   CITRATE SYNTHASE, MITO   0. 1714   49.8   460   I CISY_EMBNI   CITRATE SYNTHASE, MITO   0. 180   48.8   460   I CISY_EMST   CITRATE SYNTHASE, PERO   180   48.8   460   I CISY_EMST   CITRATE SYNTHASE, MITO   0. 1818   460   I CISY_EMST   CITRATE SYNTHASE, MITO   0. 1818   460   I CISY_EMST   CITRATE SYNTHASE, MITO   0. 1818   486   I CISY_EMST   CITRATE SYNTHASE, MITO   0. 1818   486   I CISY_EMST   CITRATE SYNTHASE   EC 2   310   37   I CISY_EMST   CITRATE SYNTHASE   EC 4   4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.	~	2021	58.7	464	↔	CISY_PIG		MITO	0.00e+00
1820   52.9   468   1   CISY_CAEEL   PROBABLE CIPRATE SYNTH   1763   51.8   482   1   CISY_CAEPT   CITRATE STUTH   0.   1763   51.8   482   1   CISY_CAEPT   CITRATE STUTHASE   STUTH   0.   1740   50.5   467   1   CISY_CANTR   CITRATE SYNTHASE, MITO   0.   1714   498   475   1   CISY_CAEPT   CITRATE SYNTHASE, MITO   0.   1714   49.8   475   1   CISY_CAEPT   CITRATE SYNTHASE, MITO   0.   1885   40.2   46.9   1   CISY_CAEPT   CITRATE SYNTHASE, MITO   0.   1885   40.2   46.9   1   CISY_CAEPT   CITRATE SYNTHASE, MITO   0.   1885   40.2   46.9   1   CISY_CAEPT   CITRATE SYNTHASE, MITO   0.   1885   40.2   40.9   40.0   40	_	1944	9	433	Н	CISY_CHICK		MITO	
1782   51.8   482   1   CISY_SCHPO   PROBABLE CITRATE SYNTH   1763   51.2   479   1   CISY_CANTR   CITRATE SYNTHASE, MITO   1725   50.1   474   1   CISY_CANTR   CITRATE SYNTHASE, MITO   1725   50.1   474   1   CISY_CANTR   CITRATE SYNTHASE, MITO   17679   48.8   460   1   CISY_CASPG   CITRATE SYNTHASE, MITO   1680   48.8   460   1   CISY_LASPT   CITRATE SYNTHASE, MITO   17818   40.2   462   1   CISY_LASPT   CITRATE SYNTHASE, MITO   17818   486   1   CISY_LASPT   CITRATE SYNTHASE, MITO   17818   486   1   CISY_LONG   CITRATE SYNTHASE   MITO   17818   486   1   CISY_LONG   CITRATE SYNTHASE   CEC   4   487   10.1   373   1   CISY_LONG   CITRATE SYNTHASE   CEC   4   486   1   CISY_LONG   CITRATE SYNTHASE   CEC   4   486   1   CISY_LONG   CITRATE SYNTHASE   CISY_LONG   180   372   1   CISY_LONG   CITRATE SYNTHASE   CEC   4   486   1   CISY_LONG   CITRATE SYNTHASE   CEC   4   4   486   CITRATE		1820	52.9	468	-	CISY_CAEEL	CITRATE	HINK	0.00e+00
1763   51.2   479   1   CISY_CEAST CITRATE SYNTHASE, MITO   1725   50.5   467   1   CISY_CANIR CITRATE SYNTHASE, MITO   1725   50.1   474   1   CISY_EMBNI CITRATE SYNTHASE, MITO   0.1   49.8   475   1   CISY_EASPI CITRATE SYNTHASE, MITO   0.1   68.0   48.8   460   1   CISY_EAST CITRATE SYNTHASE, MITO   0.1   68.0   1   CISY_EAST CITRATE SYNTHASE   10.0   0.1   68.0   0.1		1782	51.8	482		CISY_SCHPO	CITRATE	HINX	0.00e+00
1740   50.5   467   1   CISY_CANTR CITRATE SYNTHASE, MITO   1714   49	7	1763	51.2	479	Н	CISY_YEAST		MITO	0.00e+00
1725   50.1   474   1   CISY_EMENI CITRATE SYNTHASE, MITO   1719   49.8   400   1   CISY_ASPNG CITRATE SYNTHASE, MITO   1610   48.8   460   1   CISY_ASPNG CITRATE SYNTHASE, MITO   1610   48.8   460   1   CISY_INEGR CITRATE SYNTHASE, MITO   1610   48.8   460   1   CISY_INEGR CITRATE SYNTHASE, MITO   1610   48.6   1   CISY_EAST CITRATE SYNTHASE, MITO   1610   16.5   486   1   CISY_EAST CITRATE SYNTHASE   EC 4   4.3   1   CISY_BACCO CITRATE SYNTHASE   EC 4   4.4   10.1   373   1   CISY_BACCO CITRATE SYNTHASE   EC 4   4.5   10.1   373   1   CISY_BACCO CITRATE SYNTHASE   EC 4   4.5   10.1   372   1   CISY_BACCO CITRATE SYNTHASE   EC 4   5.5   1   CISY_BACCO CITRATE SYNTHASE   E	œ	1740	50.5	467	-1	CISY_CANTR		MITO	0.00e+00
1714   49.8   475   1   CISY_ASPNG CITRATE SYNTHASE, MITO   0.1627_EASPNG CITRATE SYNTHASE, MITO   0.1680   48.8   460   1   CISY_EAST CITRATE SYNTHASE, PERO   0.1680   48.2   462   1   CISY_EAST CITRATE SYNTHASE, MITO   1.218   35.4   486   1   CISY_CORGL CITRATE SYNTHASE   310   373   1   CISY_CORGL CITRATE SYNTHASE   32   2.347   10.1   373   1   CISY_BACCO CITRATE SYNTHASE   32   4.35   1   CISY_BACCO CITRATE SYNTHASE   32   4.35   1   CISY_BACCO CITRATE SYNTHASE   32   4.35   1   CISY_BACCO CITRATE SYNTHASE   33   4.35   1   CISY_SYNTA CITRATE SYNTHASE   32   4.35   1   CISY_SYNTA CITRATE SYNTHASE   33   4.35   1   CISY_SYNTA CITRATE SYNTHASE   32   4.35   1   CISY_SYNTA CITRATE SYNTHASE   33   4.35   1   CISY_STREATE SYNTHASE   34   4.35   1   CISY_PERE   CITRATE SYNTHASE   35   4.35   1   CISY_PERE   CITRATE SYNTHASE   35   4.35   1   CISY_PERE   CITRATE SYNTHASE   35   4.35	6	1725	50.1	474	۲	CISY EMENI		MITO	0.00e+00
1679   48.8   460   1   CISZ_YEAST   CITRATE SYNTHASE, PERO   0.680   48.8   469   1   CISZ_YEAST   CITRATE SYNTHASE, MITO   0.1385   40.2   46.2   1   CISY_TETH   CITRATE SYNTHASE, MITO   0.1518   35.4   486   1   CISX_YEAST   CITRATE SYNTHASE   3   CISZ_CORGL   CITRATE SYNTHASE   EC   2.347   10.1   373   1   CISY_BACCO   CITRATE SYNTHASE   EC   4.4   3.10   9.0   372   1   CISY_BACCO   CITRATE SYNTHASE   EC   4.5   3.05   8.9   372   1   CISY_BACCO   CITRATE SYNTHASE   EC   4.5   3.06   8.9   372   1   CISY_SYNTS   CITRATE SYNTHASE   EC   4.5   3.06   8.9   3.07   1   CISY_SYNTS   CITRATE SYNTHASE   EC   4.5   3.06   8.3   4.23   1   CISY_SYNTS   CITRATE SYNTHASE   EC   4.5   3.06   8.1   3.06   8.1   CISY_PERE   CITRATE SYNTHASE   EC   4.5   3.06   8.1   3.06   3	0	1714	49.8	475	~	CISY_ASPNG	-	MITO	0.00e+00
1680 48.8 469 1 CISY_NEUCR CITRATE SYNTHASE, MITO 0. 1318 540.2 462 1 CISY_TEATH CITRATE SYNTHASE, MITO 1. 1218 354 466 1 CISX_YEAST CITRATE SYNTHASE (EC 2. 350 10.5 437 1 CISY_CORGL CITRATE SYNTHASE (EC 4. 347 10.1 373 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 310 90 436 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 310 8.9 372 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 310 8.9 372 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 311 CISY_SYNTA CITRATE SYNTHASE (EC 4. 312 287 8 3 428 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 313 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 314 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 315 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 316 8.1 376 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 317 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 318 8.1 376 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 319 1 CISY_BACCO CITRATE SYNTHASE (EC 4. 310 CISY_BACCO CITRATE SYNTHASE (EC 4.	_	1679	48.8	460	7	CISZ_YEAST		PERO	0.00e+00
1385   40.2   462   1   CISY_TETTH CITRATE SYNTHASE, MITO   1.216   35.4   486   1   CISX_TEAST CITRATE SYNTHASE   3 (C. 2. 347   10.15   477   1   CISY_DAGC CITRATE SYNTHASE (EC. 4. 4. 347   1   CISY_BACCO CITRATE SYNTHASE (EC. 4. 1. 375   1   CISY_BACCO CITRATE SYNTHASE (EC. 4. 1. 376   8.9   372   1   CISY_BACSU CITRATE SYNTHASE (EC. 4. 5. 306   8.9   372   1   CISY_SYNY3   CITRATE SYNTHASE (EC. 4. 5. 307   8.3   4.23   1   CISY_SYNY3   CITRATE SYNTHASE (EC. 4. 2. 2. 4.28   1   CISY_PERE CITRATE SYNTHASE (EC. 4. 3. 4.28   1   CISY_PERE CITRATE SYNTHASE (EC. 4. 3. 4.28   1   CISY_PERE CITRATE SYNTHASE (EC. 4. 4. 3. 4.	a	1680	48.8	469	Н	CISY_NEUCR		MITO	0.00e+00
1218   35.4   486   1   CISN_YEAST CITRATE SYNTHASE 3 (EC 2. 360   10.5   437   1   CISN_CORGL CITRATE SYNTHASE (EC 4 4. 4. 4. 4. 4. 1   373   1   CISY_BACCO CITRATE SYNTHASE (EC 4 5. 310   9.0   436   1   CISY_BACSO CITRATE SYNTHASE (EC 4 5. 305   8.9   372   1   CISW_BACSO CITRATE SYNTHASE (EC 4 5. 306   8.9   397   1   CISY_SYNT3   CITRATE SYNTHASE (EC 4 3. 287   8.3   423   1   CISY_SYNT3   CITRATE SYNTHASE (EC 4 3. 4. 288   8.1   376   1   CISY_PEBAE CITRATE SYNTHASE (EC 4 1. 280   8.1   376   1   CISY_PEPAE CITRATE SYNTHASE (EC 4 1. 377   8   1   CISY_PEPAE CITRATE SYNTHASE (EC 4 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4	~	1385	40.2	462	Н	CISY_TETTH		MITO	1.50e-274
360 10.5 437 1 CISY_CORGL CITRATE SYNTHASE (EC 4 4 13.0 1 37.3 1 CISY_ACCAG CITRATE SYNTHASE (EC 4 5 13.0 9.0 4.36 1 CISY_ACCAG CITRATE SYNTHASE (EC 4 5 13.0 5.0 4.36 1 CISY_ACCAG CITRATE SYNTHASE (EC 4 5 3.0 5 8.9 37.2 1 CISY_ACCAG CITRATE SYNTHASE (II ( 5 3.0 5 8.3 4.23 1 CISY_ACCAN CITRATE SYNTHASE (EC 4 2 28.7 8.3 4.23 1 CISY_ACCAN CITRATE SYNTHASE (EC 4 1 2 28.2 8.2 4.28 1 CISY_PARCA CITRATE SYNTHASE (EC 4 1 CISY_PARCA CISTATE SYNTHASE (EC 4 1 CISTATE	4	1218	35.4	486		CISX_YEAST		) [ ]	2.04e-236
6 347 10.1 373 1 CISY_BACCO CITRATE SYNTHASE (EC 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Ŋ	360	10.5	437	П	CISY_CORGL		EC 4	4.32e-47
7 310 9.0 436 1 CISY_ACEAC CITRATE SYNTHASE (EC 4 5 3 305 8.9 372 1 CISW_BAGSU CITRATE SYNTHASE LII ( 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	و	347	10.1	373	7	CISY_BACCO		EC 4	•
8   305   8.9   372   CISW_BACSU CITRATE SYNTHASE III (   5   5   306   8.3   4.23   CISY_SINY3 CITRATE SYNTHASE (EC 4   2   2   3   3   2   2   3   3   3   3	_	310	•	436	Н	CISY_ACEAC	-	EC 4	
9 306 8.9 397 1 CISY_SYNY3 CITRATE SYNTHASE (EC 4 3 1 287 8.3 4.23 1 CISY_ACIAN CITRATE SYNTHASE (EC 4 2 2 4.28 1 CISY_PSRAE CITRATE SYNTHASE (EC 4 1 1 282 8.2 4.28 1 CISY_PYREU CITRATE SYNTHASE (EC 4 4 1 277 8 0 386 1 CISY_THIFE CITRATE SYNTHASE (EC 4 4 1 1 278_THIFE CITRATE SYNTHASE (EC 4 1 1 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	ထ	305		372	٦	CISW_BACSU		) 11:	•
0 287 8.3 423 1 CISY_ACIAN CITRATE SYNTHASE (EC 4 2 2 428 1 2182 82 428 1 CISY_PSBAE CITRATE SYNTHASE (EC 4 1 2 80 8 1 2 1 2 1 CISY_PYRFU CITRATE SYNTHASE (EC 4 4 4 4 8 1 3 8 1 CISY_PTHFE CITRATE SYNTHASE (EC 4 4 4 4 4 4 4 8 1 2 1 CISY_PTHFE CITRATE SYNTHASE (EC 4 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	σ	306		397	H	CISY_SYNY3		EC 4	
282 8 2 428 1 CISY PSEAE CITRATE SYNTHASE (EC 4 1 280 8.1 376 1 CISY_PYRFU CITRATE SYNTHASE (EC 4 4 277 8 0 384 1 CISY_THIFE CIFFALE SYNTHASE (EC 4 1	0	287	•	423	Н	CISY_ACIAN		EC 4	
280 8.1 376 1 CISY_PYRFU CITRATE SYNTHASE (EC 4 4 277 8 0 386 1 CISY_THIFE CITRATE SYNTHASE (EC 4 1	-4	282		428	П	CISY_PSEAE	-	EC 4	1.91e-31
7 8 0 386 1 CISY_THIFE CITRATE SYNTHASE (EC 4 1.81e	7	280	8.1	376	Н	CISY_PYRFU		EC 4	4.70e-31
	m	277	c 80	386	<u>, , , , , , , , , , , , , , , , , , , </u>	CISY_THIFE		EC 4	16

DB 1; Length 471;

85.2%; Score 2932;

Query Match

A7E3512D CRC32;

52183 MW;

471 AA;

40000000000000000004444444444444444444
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                                                                                                                                                                                                                                                                                                               -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBDIXT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITARIE SIS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                      CITRUS MAXIMA (PUMMELO) (CITRUS GRANDIS).
EUKARYCOTA; VIPIDIDLAMYRE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
SAPINDALES; RUTACEAE; CITRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                              THESIS (1994), UNIVERSITY OF CALIFORNIA AT RIVERSIDE, U.S.A.
CISY_CITMA STANDARD; PRT; 471 AA.
P49298;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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PROSITE: PSOOMSU; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; SCSC.
                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-CV. SIAMESE SWEET 2240;
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471
307
353
408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE: ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                         181 ALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSL 240
                                                                                                                             61 DLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDPDEGIRFRGLSIPECQKLLPAAKPDGE 120
                                                                                                                                                                61 EHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGGE 120
                                                                                                                                                                                                  121 PLPEGLLWILLTGKVPSKEQVDGLSKELRDRATVPDYVYKAIDALPVSAHPMTQFASGVM 180
                                                                                                                                                                                                                     241 DYGGNFSHMLGFDDPKMLELMRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFLAALN 300
                                                                                                                                                                                                                                                                                                                                                                    301 GLAGPLHGLANQEVLLWIKSVVDECGENVTTEQLKDYVWKTLNSGKVVPGFGHGVLRKTD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 PRYTCQREFALKHLPDDPLFQLVSKLYEVVPPILTKLGKVKNPWPNVDAHSGVLLNHFGL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVFYRGVSLLSKLRSRAVQOTNLSNSVRWLQVQTSSGLDLRSBLQELIPEQODRLKKLKS 50
                                                       1 MASLRSATALSRLRSRAGOQSNLSNSVRWLQMQSSADLDLHSQLKEMIPEQQERLKKVKS 60
                    Gaps
                                                                                                                                                                                                                                                                        181 ALQVQSEFQEAYEKGIHKSKSWEPTSEDSLNLIARVPVVAAYVYQRIYKDGKIIPKDDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNGER E.A., HAND J.M., CASHMORE A.R., VASCONCELOS A.C.; "Isolation of a cDNA encoding mitochondrial citrate synthase from Arabidopsis thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 TEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AEARYYTVLFGVSRSLGICSQLIWDRALGLPLERPKSVTLDWIEKNCKKA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLANT MOL. BIOL. 13:411-418(1989).
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                   51; Mismatches 31;
Best Local Similarity 82.3%; Pred. No. 0.00e+00;
Matches 387; Conservative 51; Mismatches 31
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01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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SUBUNIT: HOMODIMER.
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121 GLNHYRRSFVASLNWKGTL-AKSKLKH-CRKTWNRAAVSDYVYNAIDALPSTAHPMTQFA 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 DKSLDYGANFSHMLGFDDERLKELMRLTSPSTVMHEGGNVSAHTGHLVGSALSDPYLSFA
                                                                                                   LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Indels
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01-607-1989 (REL. 12, LAST SEDUNCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
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BY SIMILARITY.
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                                                                                                                                                                                       MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2454;
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
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                               PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                              52941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.3%;
Best Local Similarity 71.7%;
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                                                                                                                                           MULTIGENE FAMILY.
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P00889;
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                                                                                                                     -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBUNT: HOMODIMER.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MATPIX.
-:- CITRAIE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
            MEDLINE; 83010291.

REMINGTON S., WIEGAND G., HUBER R.;

"Crystallographic refinement and atomic models of two different forms of citrate synthase at 2.7 and 1.7-A resolution.";

J. Mol. BIOL. 158:111-152(1982).
                                                           MUTAGENESIS.
MEDLINE: 91104711.
ALTER G.M., CASAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
ALTER G.M., CASAZZA J.P., ZHI W., NEMETH P., SRERE P.A., EVANS C.T.;
ALTERGON of essential catalytic residues in pig citrate synthase.";
BIOCHEMISTRY 29:7557-7563(1990).
-i- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                    PDB: 4CTS; 16-JUL-88.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE: MITOCHONDRION; 3D-SIRUCTURE;
                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE. METHYLATION (TRI-).
       X-RAY CRYSTALLOGRAPHY (2.7 AND 1.7 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                              MITOCHONDRION
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; 1CTS; 16-JUL-88.
; 2CTS; 09-OCT-88.
; 3CTS; 09-OCT-88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 VLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPL 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 PDEGIRFRGLSIYECGKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSLSGELRSRAT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|: :|: | :||| :| |:|| :| |:|| 34 TSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGHTGLLMETSLLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 SASSINLKDILADLIPKEQARIKTFRQQHGNTVVGQITVDMMYGGMRGMKGLVYETSVLD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AKLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAOFTELMRLYLTIHSDHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 GGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2021; DB 1; Length 464; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                78; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                       51629 MW; 3BC38D25 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                           58.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265; Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                         -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-: SUBUNIT: HONODIMEN:
-! SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                            "Proposed mechanism for the condensation reaction of citrate synthase: 1.9.4 structure of the ternary complex with oxaloacetate and carboxymethyl coenzyme A."; BIOCHEMISTRY 29:2213-2219(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                          DR PDB; 1CSS; 15-OCT-95.

DR PDB; 1AL6; 24-DEC-97.

DR PDB; 1AL6; 24-DEC-97.

DR PDS; 1AL6; 24-DEC-97.

DR PRAZ: 24-DEC-97.

RW LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; 3D-STRUCTURE.

PT ACT_SITE 274 274

T ACT_SITE 375 375

T HELIX
                                                                                                                                                                                                                                                                                                                           METABOLISM.
--- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
--- CAUTION: THIS IS AN X-RAY DETERMINED SEQUENCE WHICH WAS ESTABLISHED USING THE SEQUENCE OF PIG CITRATE SYNTHASE AND MODIFYING IT BASED ON THE OBSERVED ELECTRON DENSITY.
                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF OPEN CONFORMATION
                                                         01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-AUG-1998 (REL. 36, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL (EC 4.1.3.7).
                                                                                                                                                TISSUE-HEART MUSCLE;
MEDLINE; 90248434.
KAPPUSAS M., BPANCHAUD R., REMINSTON S J.;
                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                          PRT;
                                                                                                      GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320
375
375
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375
477
470
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80
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15-APR-91.
15-APR-91.
15-APR-91.
24-DEC-97.
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2CSC; 15-APR-91
||||||: :
ERPKSVIME 460
                                                                                                                                                                                                                                                                                  OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 4
CISY_CHICK
P23007;
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50SC;
60SC;
50TS;
60TS;
10SH;
10SI;
10SR;
10SS;
1AL6;
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61 DEGIRFRGFSIPECOKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWARRAAL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 LRDYIMNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPGDPMFKLVAQLYKIVPNV 360 | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 334 LKDYAMKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 QVPLVAAYVYRRMYKNGNTI-PKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHEG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGADAS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLEQGAAANPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 DEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLMLLLTGKVPSKEQVDSLSQELRSRATV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASSTNLKDVLAALIPKEQARIKTFRQQHGGTALGQITVDMSYGGMRGMKGLVYETSVLDP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 SSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1944; DB 1; Length 433;
Pred. No. 0.00e+00;
73; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47373 MW; 6E24FE58 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.3%;
Matches 258; Conservative
 375
374
375
385
385
390
415
427
433 AA;
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444 MGLPLERPKSHSTD 457
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319
365
420
482 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                               CISY_SCHPO
Q10306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPAC6C3.03
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 SRAIVPDHVYKTIDALPVIAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 SVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 ARADLPTHVVRMLDNFPDNLHPPMAQFIAAIANLNESKFAGAYARGVAKASYWEYAYEDS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 MDLLAKLPIVAAIIYRNLYRDGSAVSVIDPKKDWSANFSSMLGYDDPLFAELMRLYLVIH 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 MSLIAQVPLVAAYVYRRMYKNGNTIP-KDDSLDYGANFAHMLGFSSSDMHELMKLYVTIH 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 SDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGFN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P23007; 5CSC. TYPOTHERICAL PROTEIN: LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 LSTSAEGSTNLKEVLSKKIPAHNAKVKSFRTEHGSTVVQNVNIDMIYGGMRSMKGMVTET 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.00e+00;
82; Mismatches 103; Indels 4; Gaps
                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                             01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
BERKS M., SMITH A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRAIE + COA = ACETYL-COA + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1820; DB 1; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i. ADA3A630 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WORMPEP; T20G5.2; CE00513.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                                                                                                                      01-FEB-1994 (REL. 28, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00285; citrate_synt;
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1 Similarity 56.5%;
245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z30423; G458482; -.
                                                                                              STANDARD;
                                                                                                                                                                                                                                                            CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S42370; S42370
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453 RPKSVTME 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METABOLISM.
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                                                                                       CISY_CAEEL P34575;
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ACT_SITE
SEQUENCE
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Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 VFLQFLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGIC-SQLIWDRA 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 FRGYTIPECQKLLPSSPNGKQPLPESLFWLLVTGEIPTLSQVQALSADWAARSQLPKFVE 170
269 SDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANGEVLLMIKSVVEECGEN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P23007; SCSC.
HYPOTHETICAL PROTEIN; LYASE; TRICARBOXXLIC ACID CYCLE; MITOCHONDRION;
                                                                                                          325 YTEEQLKEWVWKHLKSGQVVPGYGHAVLRKTDPRYECQREFALKHLPNDDLFKLVSTLYK 384
                                                                                                                                                                              329 ISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 LPSELQELIPEQQDFLKKLKSEHGKVQLGNITVDMVLGGMPGMTGLLWETSLLDPDEGIR 99
                                                                                                                                                                                                                                                   385 ITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALG-CLSQLIWARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-972;
DEPLIN K., CHURCHER C.M., BAPRELL B.G., RAJANDREAM M.A., WALSH S.'
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYIIC ACTIVITY: CITRAIE + COA - ACETYL-COA + H(2)O +
OXALOACETAIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION (BY SIMILARITY).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 18145A7D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1782; DB 1; Length 482;
Pred. No. 0.00e+00;
83; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 51.8%; Score 1782; Local Similarity 57.2%; Pred. No. 0.0 es 242; Conservative 83; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z69731; E223710; -.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54030 MW;
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482
319
365
420
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PATHWAY: TRICARBOXYLIC ACID CYCLE.
SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                  160 KTIDALPVTAHPMTQFATGVWALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLV 219
                                                                                                                                                                                291 HIGHLVGSALSSPFLSMAASLNGLAGPLHGLANQEVLNFLITMKKEIGDDLSEETIKSYL 350
                                                                                                                                                                                                                                                                                                                                                                                                                       351 WKLLNSGRVVPGYGHAVLRKTDPRYTAQREFALEHLPKDPMFQLVSRLYEIVPGVLTEHG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 KTKNPYPNVDSHSGVLLQYYGLKEQSFYTVLFGVSRTLGVASQLIWDRALGLPIERPKSF 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 KL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGICSOLIWDRALGLPLERPKSV 457
171 ELIDRCPPTLHPMAQFSLAVTALEHDSAFAKAYERGMNKHDYWKYEYEDCMDLIAKTVPI 230
                                                                                                                                                                                                                                                                                                                                                 279 HTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYA 338
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"Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right
                                                                                                                                           231 AGRIYRNLYRDGVVAPIQMDKDHSYNFANVLGFANNEEFVELMRLYLTIHADHEGGNVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUISSA M., SUDA K., SCHATZ G.;
Isolation of the nuclear yeast genes for citrate synthase and
fifteen other mitochondrial proteins by a new screening method.";
EMBO J. 3:1773-1781(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALO D., STETTLER S., MARIOTTE S., GENDREAU E., THURLAUX P., "Organization of the centromeric region of chromosome XIV in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.";
YEAST 10:523-533(1994).
-!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (REL. 01, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
CITRATE SYNTHASE (BAKEN'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-D273-10B;
LINDNER P., PLUECKTHUN A ;
SUBMITTED (JUL-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SACCHAROMYCETACEAE; SACCHAROMYCES.
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MEDLINE; 95028151.
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P00890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 IPEHVIQLLDSLPKDLHPMAQFSIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 GNVSAHTTHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLEWLFKLREEVKGDYSKET 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 IEKYLWDTLNAGRVVPGYGHAVLRKTDPRYTAQREFALKHFPDYELFKLVSTIYEVAPGV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 LIKHGKIKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGAPIE 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 PEEGIRFRGRTIPEIQRELPKAEGSTEPLPEALFWLLLTGEIPTDAQVKALSADLAARSE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 SASEQTLKERFAEIIPAKAEEIKKFKKEHGKTVIGEVLLEQAYGGMRGIKGLVWEGSVLD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 TSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88; Mismatches 102; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKLPVIASKIYRNVFKDGKITSTDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDHEG
                                                                                                                                                                                                                                                                                                                   LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 479;
-!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                  CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
E -> Q (IN REF. 2).
E -> EE (IN REF. 2).
W; C6896385 CRC32:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.00e+00;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1763;
                                                                                                                                                                                                                                                                   PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
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38 479 CIT
312 312 BY
358 358 BY
413 413 BY
78 78 E
479 AA; 53360 WW; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 55.4%;
hes 237; Conservative
                                                                                                                                                        EMBL; Z23259; G313750; -.
                                                                                                                                                                         EMBL; X00782; G3603; -.
EMBL; X77395; G496718; -.
EMBL; Z71616; E239778; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                      PIR; A01110; YKBY.
PIR; S35390; S35390.
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                                                                                                                                                                                                                                                       SGD; L0000341;
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P79024;
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ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 EVPTEAQTRALSEEFAARSALPKHVEELIDRSPSHLHPMAQFSIAVTALESESQFAKAYA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 KGVHKSEYWKYTYEDSIELLAKLPTIAAKIYRNVFHDGKLPAQIDSKLDYGANLASLLGF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 GENKEFLELMRLYLTIHSDHEGGNVSAHTTHLVGSALSSPFLSLAAGLNGLAGPLHGPAN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 QEVLEWLFKLREELNGDYSKEAIEKYLWDTLNAGRVGPGYGHAVLRKTDPRYTAQREFAL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 QAYGGMRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLPEALFWLLLTG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 MVLGGMRGMTGLLWETSLLDPDEGIRFRGLSIYECQKVLPAAKPGGEPLPEGLLWLLIG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 KVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 SSS-DMHELMKLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLAN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 QEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFAL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 KHMPDYELFKLVSNIYEVAPGVFDQHGMTK-NPWPNVGSHSGVLLQYYGLTEESFYTVLF 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 RSSNVAKSTLKNSVR--TYATAEP-TLKQRLEEILPAKAEEVKQLKKDYGKTVIGEVLLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 RSRAVQQTNLSNSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Mismatches 111; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; FUNGI; ASCOMYCÓTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.

1 ANTOCHOMBETAN 'ACCESSION' PEPTIDE.
                                                                                                                                                                               UEDA M., SANUKI S., KAWACHI H., SHIMIZU K., ATOMI H., TANAKA A SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION (POTENTIAL).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1740; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEE342A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 GVSRAFGVLPQLILDRGLGMPIERPKSFSTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00480; CITRATE SYNTHASE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB001565; G1871439; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 50.5%;
Local Similarity 55.4%;
                                                        CANDIDA TROPICALIS (YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467
                                                                                                 CANDIDACEAE; CANDIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
347
3402
467 AA;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            OXALOACETATE
                                                                                                                                                                                                                                                                                                                        METABOLISM.
                                                                                                                                                              STRAIN-PK233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 KIIDALPVTAHPMIQFATGVMALQVQSEFQKAYEKGIHKSKLWEPIYEDSMSLIAQVPLV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 AAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSS-DMHELMKLYVTIHSDHEGGNVSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 ELIDRVPSTLHPMAQFSLAVTALEHESAFAKATAKGINKKDYWNYTFEDSMDLIAKLPTI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 AAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGFADNKDFVELMRLYLTIHSDHEGGNVSA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTEMKKVVGNDLSDQSIKDYL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 HTGHLVASALSDPYLSFAAALNGLAGPLHGLANOEVLLWIKSVVEECGENISKEOLKDYA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 LKETFADKLPGELEKVKKLPKEHGNKVIGELTILDQAYGGAPGVKCLVWEGSVLDSEEGIP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 FRGLTIPECQKLLPKAPGGEEPLPFGLFWLLLTGEVPSEQQVRDLSAEWAARSDLPKFIE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 LRSELOELIPEQODRLKKLKSEHGKVOLGNITVDMVLGGMRGMTGLLWETSLLDPDEGIR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                PARK B.W., HAN K.H., LEE C.Y., LEE C.H., MAENG P.J.;
"Cloning and characterization of the citA gene encoding the
mitochondrial citrate synthase of Aspergillus nidulans.";
MOL. CELLS 7:290-295(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 474;
                                                                                                                                                                                                                                                                          EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; EMERICELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRION (POTENTIAL).
CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITPATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4 1.3.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1725; DB 1;
Pred. No. 0.00e+00;
79; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D97E1E91 CRC32;
                                  474 AA
                                                                                                                                                                                                                                          EMERICELLA NIDULANS (ASPERGILLUS NIDULANS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00480; CITRATE_SYNTHASE; 1. PFAM; PF00285; citrate_synt; 1. HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: TRICAPBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 57.4%;
les 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U89675; G2138332; -.
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474
310
356
411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 AA;
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-FGSC 4;
MEDLINE; 97306446.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356
411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METABOLISM.
LI 9
CISY_EMENI
O00098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: TRICARBOXYLIC ACID CYCLE.
SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                461
                                                                                      95 DSEEGIRFRGRTIPECQELLPKA-PGGQEPLPEGLFWLLLTGEIPTEQQVRDLSAEWAAR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 SDLPKFIEELIDRCPSTLHPMSQFSLAVTALEHESAFAKAYAKGINKKDYWNYTFEDSMD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AIVPDHVYKTIDALPVIAHPMIQFAIGVMALQVQSEFQKAYEKGIHKSKLWEPIYEDSMS 211
342 WSTLNAGRVVPGYGHAVLRKTDPRYTSQREFALRKLPDDPMFKLVSQVYKIAPGVLTEHG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 TGKAKSLKETFAEKLPAELEKVKKLRKEHGSKV-IGEVTLDQAYGGARGVKCLVWEGSVL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 TSSGLDLFSELQELIPEQODFLKKLKSEHG-KVQLGNITVDMVLGGMRGMTGLLWETSLL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; MITOSPORIC TRICHOCOMACEAE; ASPERGILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 DPDEGIRFRGLSIYECQKVLPAARPGG-EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSR
                                                                       402 KIKNPYPNVDAHSGVLLQYYGLIERNYYTVLFGVSRALGVLPQLIIDRAFGAPIERPKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSHIDA Y., MIYAKE K., KANAYAMA S., KIRIMURA K., USAMI S.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1714; DB 1; Length 475; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99; Indels
                                                                                                                                                                                                                                                                                 01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SECUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Mismatches
                                                                                                                                                                                                                                                 475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 49.8%;
Local Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246; Conservative
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D63376; G927641; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           ASPERGILLUS NIGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-WU-2223L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METABOLISM.
                                                                                                                                        462 STE 464
                                                                                                                                                                            458 TME 460
                                                                                                                                                                                                                                               CISY_ASPNG
P51044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
ACT_SITE
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-i- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                            | SECTION | SECT
                                                                                                                                                    274 HEGGNVSAHTTHLVGSALSSPMLSLAAGLNGLAGPLHGLANQEVLNWLTKMKAAIGNDLS 333
                                                                                                                                                                                                                                                                                                             334 DEAIKNYLWSTLNAGQVVPGYGHAVLRKTDPRYVSQREFALRKLPDDPMFKLVSQVYKIA 393
                                                                                                                                                                                                                                                                                                                                                                                     331 KEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVF 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 PGVLTEHGKIKNPYPNVDAHSGVLLQYYGLTEANYYTVLFGVSRALGVLPQLIIDRALGA 453
214 LIAKLPTIAAKIYRNVFKDGKVAPIQKDKDYSYNLANQLGYGDNNDFVELMRLYLTIHSD 273
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SACCHAROMYCETACEAE; SACCHAROMYCES.
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BITEAU N., FREMAUX C., HEBRARD S., MENARA A., AIGLE M., CROUZET "The complete sequence of a 10.8kb fragment to the right of the chromosome III centromere of Saccharomyces cerevisiae."; YEAST 8:61-70(1992).
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LIAO X., SMALL W.C., SRERE P.A., BUTOW R.A.;
LIAO X., SMALL W.C. SRERE P.A., BUTOW R.A.;
LIATAMILOCHONDYIAI functions regulate nonmitochondrial citrate synthase (CIT2) expression in Saccharomyces cerevisiae.";
MOL. CELL. BIOL. 11:38-46(1991).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
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ROSENKRANTZ M., ALAM T., KIM K.-S., CLARK B.J., SRERE P.A.
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01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITEARIE SYNTHASE, PEROXISOMAL (EC 4.1.3.7).
CITZ OR YCROUSC OR YCRSC OR YCROUS.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S5 LLWETSLLDPDEGIRFRGLSIXECQKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEQVDSL 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 NSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92; Mismatches 115; Indels 1; Gaps
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"Characterization of the cit-1 gene from Neurospora crassa encoding
"Characterization of the cit-1 gene from Sucrospora crassa encoding
the mitochondrial form of citrate synthase.";
MOL. GEN. GENET. 242:105110(1994).
--- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MICROBODY TARGETING SIGNAL (POTENTIAL) 9E93E2FD CRC32;
                                                                                                                                                                                                                                                                                                                      TRICARBOXYLIC ACID CYCLE; PEROXISOME; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 460;
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SORDARIALES; SORDARIACEAE; NEUROSPORA.
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Pred. No. 0.00e+00;
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                      PROSITE: PS00342; MICROBODIES_CTER, 1.
PROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt; 1.
HSSP; P23007; 5CSC.
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01-FEB-1994 (REL. 28, LAST SEQI
01-NOV-1995 (REL. 32, LAST ANN
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Local Similarity 52.4%;
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                          EMBL; X59720; E264468;
PIR; A25393; YKBYC.
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                                                                                                  YEPD; 5440; -.
SGD; L0000342; CIT2.
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.
                                  FARMAN, TALCALLOLAR LOCATION. MITOCHONDRIAL MATRIX.
DEVELOPMENTAL CSTAGE: ABBUDANT AFTER 6-12 HRS OF GROWTH, IT IS
NOT SIGNIFICANTLY EXPRESSED AFTER 24 HRS, WHICH IS SEVERAL HRS
AFTER ENTERING THE STATIONARY PHASE OF GROWTH.
CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 YLWDILNAGRVVPGYAHAVLRKIDPRYSAQRKFAQEHLPEDPMFQLVSQVYKIAPKVLTE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 HGKTKNPYPNVDAHSGVLLQHYGLTEANYYTVLFGVSRAIGVLPQLIIDRAVGAPIERPK 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 RFRGKTIPECQELLPKA-PGGKEPLPEGLFWLLLTGEVPSEQQVRDLSAEWAARSDVPKF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 IEELIDRCPSDLHPMAQLSLAVTALEHTSSFARAYAKGINKKEYWGYTFEDSMDLIAKLP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 VYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 TIAARIYQNVFKGGKVAAVQKDKDYSFNFANQLGFGDNKDFVELLRLYLTIHTDHEGGNV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 SAHTTHLVGSALSSPFLSVAAGLNGLAGPLHGLANOEVLNWLTEMKKVIGDDLSDEAITK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 LKERFAELLPENIEKIKALRKEHGSKV-VDKVTLDQVYGGARGIKCLVWEGSVLDAEEGI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 LRSELQELIPEQQDRLKKLKSEHG-KVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.8%; Score 1680; DB 1; Length 469;
larity 56.2%; Pred. No. 0.00e+00;
Conservative 78; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                    METABOLISM. SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
E6281B97 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CISY_TETTH STANDARD; PRT; 462 AA. P24118; 01-WAR-1992 (REL. 21, CREATED) 01-WAR-1992 (REL. 21, LAST SEQUENCE UPDATE) 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_synt; 1.
HSSP; P23007; 5CSC.
                    PATHWAY: TRICARBOXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 33 MI
34 469 CI
352 352 BY
469 AA; 52002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M84187; G168775; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 SYSTDKWIEI-CKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 SVTME-WLENHCKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S41563; S41563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 12; Gaps 10;
                                                                                                                                                                                                                                                                                                    CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKG-IHKSKLWEPTYEDSM 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 DLIAKIPRVAAIIYRHKYRDSKLIDSDSKLDWAGNYAHMMGFEQHVVKECIRGYLSIHCD 263
                                        EUKARYOTA; ALVEOLATA; CILIOPHORA; OLIGOHYMENOPHOREA; HYMENOSTOMATIDA;
TETRAHYMENINA; TETRAHYMENA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 IIFRGYTIPQLKEFLPKADPKAADQANQEPLPEGIFWLLMTGQLPTHAQVDALKHEWQNR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 IRFRGLSIYECQKVLP-A-AKPG--G--EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 GTVNQDCVNFILNLPKDLHSMTMLSMALLYLQKDSKFAKLYDEGKISKKDYWEPFYEDSM 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 SLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 HEGGNVSAHTTHLVGSALSDPYLSYSAGVNGLAGPLHGLANQEVLKWLLQFIEEKGTKVS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 HEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENIS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 DKDIEDYVDHVISSGRVVPGYGHAVLRDTDPRFHHQVDFSKFHLKDDQMIKLLHQCADVI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 NLKKVIAEIIPQKQAELKEVKEKYGDKV-VGQYTVKQVIGGMRGMKGLMSDLSRCDPYQG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 DLRSELQELIPEQQDRLKKLKSEHG-KVQLGNITVDMVLGGMRGMTGLLWETSLLDPDEG 97
                                                                                                                                                                  BIOCHEM. BIOPHYS. RES. COMMUN. 174:1028-1034(1991).
-!- FUNCTION: STRUCTURAL PROTEIN INVOLVED IN ORAL MORPHOGENESIS AND IN PRONUCLEAR BEHAVIOR DURING CONJUGATION. RESPIRATORY ENZYME.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                              NUMATA O., TAKEMASA T., TAKAGI I., HIRONO M., HIRANO H., CHIBA J.,
WATANABE Y.;
                                                                                                                                           "Tetrahymena 14-nm filament-forming protein has citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX AND CYTOPLASMIC
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 462; 50e-274;
                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
7; 7B6A39BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION
                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 22-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JN0130; JN0130.
PROSITE: PSO0480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                            PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               So.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 40.2%;
Local Similarity 49.0%;
es 215; Conservative
             FILAMENT-FORMING PROTEIN).
TETRAHYMENA THERMOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D90117; E33571; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 AA;
                                                                                                  91128358
                                                                                                                                                                                                                                                                                        CYTOSKELETON.
                                                                                                                                                                                                                              OXALOACETATE
                                                                                                                                                                                                                                                                                                                   METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOSKELETON
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
SEQUENCE
                                                                                                                                                          activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                         391 LQFLQNLAKL-NPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSRALGIC-SQLIMDRALG 448
331 KEQLKDYAWKTLKSGKVVPGFGHGVLRKTDPRYTCQREFALKHLPEDPLFQLVAKLYEVF 390
                                                          384 PKKLLTYKKIANPYPNVDCHSGVLLYSLGLTEYQYYTVVFAVSRALG-CMANLIWSRAFG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 315 BY SIMILARITY.
361 361 BY SIMILARITY.
419 419 BY SIMILARITY.
484 486 MICRORODY TARGETING SIGNAL (POTENTIAL).
486 AA: 53811 MM; 806F987D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , WALSH S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WANG Y., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D., HALL J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STORMS R.K., VO D.H., WINNETT E.;
SUBMITTED (XXX-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C / AB972;
PEARSON D , ROWMAN S., BARPELL, B G., RAJANDREAM M.A.,
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JIA Y.K., BECAM A.-M., SLONIMSKI P.P., HERBERT C.J.; SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRICARBOXYLIC ACID CYCLE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%; Score 1218; DB 1, 45.0%; Pred. No. 2.04e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                              (REL. 32, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                           486 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRICARBOXYLIC ACID CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: 248951; G763000; -.
EMBL: Z71255; E236811; -.
EMBL: U31900; G399735; -.
SGD: L0002855; CIT3.
PROSITE; PS00342; MICROBODIES_CTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00480; CITRATE_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00285; citrate_synt; 1.
HSSP; P23007; 5CSC.
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (REL. 32, CREATED)
                                                                                                                                                                             443 LPIERPGSADLKWFHDKYR 461
                                                                                                                                                                                                                                  449 LPLERPKSVIMEWLENHCK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITRATE SYNTHASE 3 (EC 4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205; Conservative
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                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CW04
                                                                                                                                                                                                                                                                                                                                                 CISX_YEAST
P43635;
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21 IIKSSALTLKEALENVIPKKRDAVKKLKACYGSTFVGPITISSVLGGMRGNQSMFWQGTS 80

LYASE; TRICARBOXYLIC ACID CYCLE; ALLOSTERIC ENZYME.
ACT\_SITE 316 BY SIMILARITY.
ACT\_SITE 372 BY SIMILARITY.

437 AA; 48929 MW; B408BFA5 CRC32;

SEQUENCE

FT SO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- ENZYME REGULATION: WEAKLY INHIBITED BY ATP (APPARENT KI = 10 MM).
-:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBBULT: HOMOHEXAMER (BY SIMILARITY).
-:- CUTRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                             LDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELAI 140
                                                                                                                                                                     LDPDEGIRFRGLSIYECQKVLPAAKPGGEP-LPEGLLWLLIGKVPSKEQVDSLSQELRS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVVRFLIEMNSNIS-SIAREQEIKDYLWKILNSNRVIPGYGHAVLRKPDPRFTAMLEFAQ 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 KRPIEFENDKNVLLMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLFFTV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95005436.

EIKMANNS B.J., THUM-SCHMITZ N., EGGELING L., LUEDTKE K.U., SAHM H.;

"Nucleotide sequence, expression and transcriptional analysis of the
Corprebacterium glutamicum gltA gene encoding citrate synthase.";

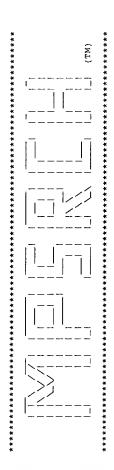
MICROBIOLOGY 140:1817-1828(1994).

-:- CATALYIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +

OXALOACETATE.
|::||i :||::: :| : ::|: : :| :|: :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :| 
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ACTINOMYCETALES; CORYNEBACTERINEAB; CORYNEBACTERIACEAE;
CORYNEBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 IFGCSRAMGPLTQLVWDRILGLPIERPKSLNLEGLE 475
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORYNEBACTERIUM GLUTAMICUM
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EMBL: X66112; G505581; -.
PROSITE: PSO0480; CITRATE\_SYNTHASE; 1.
PFAM: PF00285; citrate\_synt; 1.
HSSP; Q53554; 1A.8.

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22;
                                                                                                    97 LLINGELPTPDELHKFNDEIRHH-TLLDEDFKSQFNVFPRDAHPMATLASSVNILST-Y- 153
                                                                                                                                       129 LLLTGKVPSKEQVDSLSQELRSRATVPDHVYKT-IDALPVTAHPWIQFATGVMALQVQSE 187
                                                                                                                                                                                                                              248 HML-GFSS-S-DMHELM-K-L--YVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 300
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                                                                                                                                                                                                                                                                                                                                                                                                          267 ALSGPLHGGANQAVLEMLEDIKSNHGGD-ATEFMNK-V-KNKEDGVRLMGFGHRVYKNYD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 PRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALA-DDYFISRKLYPNVDFYTGLIYRAM 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 YQDQLN-PLDEAQL-D-K--ATVRLMAKVPMLAAYAHPAR-KGAPYMYPDNSLNARENFL 207
                                                    89; Mismatches 105; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                           RWMFGYPTEPYEIDPIMVKALDKLLILHADHEQ-NCSTSTVRMIGSAQANMFVSIAGGIN
       Length 437;
                             Pred. No. 4.32e-47;
     Score 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: Fri Oct 22 17:07:24 1999 Job time : 64 secs.
Match 10.5%;
Local Similarity 30.4%;
les 96; Conservative
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     Query Match
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Oct 22 17:07:42 1999; MasPar time 29.55 Seconds 866.114 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-702-718-6 (1-469) from US08702718.pep Title:

Description: Perfect Score:

3443 1 MVFYRGVSLLSKLRSRAVQO.....PLERPKSVTWEWLENHCKKA 469 Sequence:

Scoring table:

179066 seqs, 54579741 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

sptremb19
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 49.645; Variance 97.075; scale 0.511 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result No.	Score	Query Match	Query Match Length DB	ΩI	Description	Pred. No.
e	3443	100.0	469 10	024135	CITRATE SYNTHASE (EC 4	0.00e+00
2	3098	0.06	471 10	043175	ETHANOLAMINE AMMONIA-L	0.00e+00
ĸ	3096	6.68	472 10	080433	CITRATE SYNTHASE (EC 4	0.00e+00
4	2987	86.8	474 10	064869	CITRATE SYNTHASE (EC 4	0.00e+00
S	2800	81.3	437 10	096544	CITRATE (SI)-SYNTHASE	0.00e+00
9	2131	61.9	339 10	024259	CITRATE (SI)-SYNTHASE	0.00e+00
7	1997	58.0	466 4	075390	CITRATE SYNTHASE (EC 4	0.00e+00
80	272	7.9	372 1	028929	CITRATE SYNTHASE (CITZ	7.31e-28
on.	264	7.7	379 1	032705	CITRATE SYNTHASE (EC 4	
10	260	7.6	379 2	034002	CITRATE SYNTHASE.	1.14e-25
11	253	7.3	411 2	053115	CITRATE SYNTHASE (FRAG	2.11e-24
12	251	7.3	411 2	059777	CITRATE SYNTHASE (EC 4	4.83e-24
13	250	7.3	411 2	P77936	CITRATE SYNTHASE (EC 4	7.32e-24
14	252	7.3	431 2	033066	CITRATE SYNTHASE (EC 4	3.19e-24
15	247	7.2	411 2	060047	CITRATE SYNTHASE (EC 4	2.54e-23
16	246	7.1	411 2	059469	CITRATE SYNTHASE (EC 4	3.83e-23
17	245	7.1	411 2	059779	CITRATE SYNTHASE (EC 4	5.80e-23
18	243	7.1	411 2	059775	CITRATE SYNTHASE (EC 4	1.32e-22
19	241	7.0	410 2	059769	CITRATE SYNTHASE (EC 4	3.01e-22
20	238	6.9	356 2	054382	CITRATE SYNTHASE (EC 4	1.03e-21

1.20e-20	1.80e-20	1.70e-17	4.42e-14	9.61e-13	6.43e - 12	6.43e-12	2.06e-12	2.06e-12	9.39e-12	2.91e-11	2.73e-10	1.81e-03	1.81e-03	1.42e-01	2.57e-01	6.19e - 01	8.26e-01	2.57e+00	1.94e+00	1.46e + 00	1.94e + 00	υ.	2.57e+00	1.10e+00		
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469	SNCE	A; E COPE	TZE	1 >	TASE	core 3443; DB red. No. 0.00e+ 0; Mismatches	OTSS 1111 OTSS	OPDE IIII	rvpi 
7	SQUI	HYTZ NOL:	ELM.	COA	E SYNTHAS  [ASE; 1. ].  (BE3C325	344 No 15m2	× – ×	SLLI	SRA
PRT;	ATEI T SI	CO) TOP!	į s	+ 5 2	ASE SO	e e e	VRW.	WET 	ELR   ELR
D.	CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	CITI.  NICOTIANA TABACUM (COMMON TOBACCO).  NICOTIANA TABACUM (COMMON TOBACCO).  EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TR  EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYL  ASTERIDAE: SOLANMAE: SOLAMALES: SOLAMACEAE: NICOTIAMA.	COM N.A. SNN; U., LANDSCHUETZE V., PHYSTOI. 0.0-0/01	-! - CATALYTIC ACTIVITY: CITRATE + COA = OXALOACETATE! PATHWAY: TRICARBOXYLIC ACID CYCLE! CITRATE SYNTHAME TO FOUND IN NEARLY	CIRCLE SIMILABLISM. OXIDATIVE METABOLISM1. SIMILARITY: TO OTHER CITRATE SYNTHASES EMEL, X46.226; E137432; -1. PROSITE; PSO0480; CITRATE_SYNTHASE; 1. PRAM; PF00285; CITRATE_SYNTHASE; 1. PRAM; PF0785; CITRATE_SYNTHASE; 1. STANS: TROCARBOXYLIC ACID CYCLE. SEQUENCE 469 AA: 52492 MW: 66B33C325 CR	Score 3443; DB 10; Pred. No. 0.00e+00; 0; Mismatches 0;	MVFVRGVSLLSKLRSRAVQQTNLSNSVRWLQVQTSSGLDLRSELQELIPEQQDRLKKLKS 	EHGKVOLGNITVDMVLGGMRGMTGLLMETSLLDPDEGIRFRGLSIVECOKVLPAAKPGGE 	PLPEGLLMLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVM 
	01-74N-1998 (TREMBLREL. 05, CR 01-JAN-1998 (TREMBLREL. 05, LA 01-NOV-1998 (TREMBLEEL. 08, LA CTTRATE, SYWHASE, FR. 4.1.3, 7).	ST ST	ZE	CAN	CITRA CITRA SYNT TT; 1		H H	GMT CGMT	SQX 
.; Σ		MON AE;		KEL	LSF.  LISM.  THER C  2; -:  TRATE.  te_syn  ACID	0.0% 0.0%	00 - N	GMF 	XKEC  -
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PRELIMINARY;	(TREMBLREL. (TREMBLREL. (TREMBLREL.	CITI.  NICOTIANA TABACU EUKARYOTA; VIRID EUPHYLLOPHYTES; ASTERIDAE: SOLAN	SEQUENCE FROM N.A. STRAIN-CV. SNN; LA COGNATA U., LAN DIANT CFII, PHYSTOL	CATALYTIC AC OXALOACETATE PATHWAY: TRI	OXIDATIVE METRACLISM.  -1. SIMILARITY: TO OTHER.  EMBL: X84226: E137432.  -2. FROSITE: PSO0480; CITRARE.  PRAM: PF00285: CITRARE.  PRAM: PF00285: CITRARE.  PLAME: TRICARROXILIC ACID.  SEQUENCE 469 AA: 55492.	Ouery Match 100.0%; Best Local Similarity 100.0%; Matches 469; Conservative	SLL	GNI	WLL.
	8 6 0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	TA)	Y SI	YTI ACE	1224 1226 1226 1028 1038	imi 9;	RGV       RGV	\$-\$ 5-5	GLE
	024133; 01-JAN-1998 01-JAN-1998 01-NOV-1998 CITRATE SYNT	ANA OIA CLOP	[1] SEQUENCE FROM N STRAIN-CV. SNN; LA CGGNATA U., PLANT CELL DHVS	ALO	MIL MIL X84 E; E; TR	1 S	VFY      VFY	HGK    HGK	1 - 1 - 2 - 3
135	JAN JAN NOV	11. OTI ARY HYL	COG	SSAL	OXIDO OXIDO EMBL; X8 PROSITE; PFAM; PFI LYASE; TI	Mat Loca	<b>Σ-Σ</b>	61 E	121 P
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120 EPLPEGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHV-YKTIDALPVTAHPWTQFATG 178
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                                                                                      DYGANFAHMLGFSSSDMHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 300
                                                                                                            241 DYGANFAHMLGESSSDMHELMKLYVT1HSDHEGGNVSAHTGHLVASALSDFYLSFAAALN 300
                                                                                                                                                                       GLAGPLHGLANOEVLLWIKSVVEECGENISKEOLKDYAWKTLKSGKVVPGFGHGVLRKTD 360
                                                                                                                                                                                                             301 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTD 360
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                                                                                                                                                                                                                                                                               61 SDM-KGSIGNITVDMVLGGMRGMTGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LANDSCHUETZE V . WILLMITZEP L , MUELLER-ROEBER B .: "Micochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds."; PLANTA 196:756-764(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOLANUM TUBEROSUM (POTATO).

SULANUM TUBEROSUM (POTATO).

SURARYOTA, VIRLIDELANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERWATOPHYTA, MAGNOLIOPHYTA; EUDICOTYLEDONS; ASTERTDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
ALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 3098; DB 10; Length 471; 89.6%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ETHANOLAMINE - ACETALDEHYDE + NH(3).
-!- COFACTOR: COBALAMIN.
-!- COFACTOR: COBALAMIN.
-!- CATALOTOR: COBALAMIN.
-!- CATALOTOR: CATALOMIN.
-!- CATALOTOR: CATALOMIN.
-!- CATALOTOR: ACTIVITY I.
--- COFACTOR: SOLTU: 2977; mn15200.
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01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
ETHANOLAMINE AMMONIA-LYASE (EC 4.3.1.7).
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23; Mismatches
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Conservative
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                                                                                                                         358 KTDPRYTCQREFALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
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300 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYVWKTLNSGKVVPGFGHGVLR 359
                                       298 ALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
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                                                                                                                                                                                      GLTEARYYTVLFGVSRALGICSQLIWDRALGLPLERPKSVTMEWLENQCKKA 471
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ASTERIDAE; ARALIALES; APIACEAE; DAUCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.9%; Score 3096; DB 10; Length 472; 86.2%; Pred. No. 0.00e+00; vative 46; Mismatches 17; Indels 2
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TAKITA E., KOYAMA H., SHIRANO Y., SHIBATA D., HARA T.;
TAKITA E., KOYAMA H., SHIRANO Y., SHIBATA D., HARA T.;
STBAI encoding carrot mitochondrial citrate synthase.";
SUBNITED (AUG-1998) TO EMBL/CEBRANK/DBJ DATA BANKS.
-:- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O
                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 AA; 52656 MW; D46C38CC CRC32;
                                                                                                                                                                                                                                                                                           472 AA
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BMBL; ABOIT159; D1033521. -.
PROSITE: PSO0480; CITRATE_SYNTHASE; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
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                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DAUCUS CAROTA (CARROT)
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPRYVCQREFALKHLPDDPLFQLVSKLYEVVPPVLTELGKVKNPWPNVDAHSGVLLNHYG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEGIRFRGLSIPECQKVLPTAQSGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKT 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
ROUNGLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KALL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VERTER J.C.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
   421 LTEARYYTVLFGVSRAIGICSQLVWDRALGLPLERPKSVTMEWLENHCKKS 471
                                       419 LIEARYYTVLFGVSRALGICSQLIWDRALGLPLERPRSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 LIEARYYTVLFGVSRSLGICSQLIWDRALGLALERPKSVTMDWLEAHCKKA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Mismatches 27; Indels
                                                                                                                                                                                                                                                                   01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2987; DB 10;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL, AC004521; G3128180; -.
PROSITE; PS00480; CITRATE_SYNTHASE; 1.
LYASE; TRICARBOXIC ACID CYCLE.
SEQUENCE 474 AA; 52782 MW; 64FF2AC6 CRC32;
                                                                                                                                                                                                          474 AA
                                                                                                                                                                                                                                                                                                                                                                                                         ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                            CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389; Conservative
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OXALOACETATE
                                                                                                                                                                      LT 4
064869
                                                                                                                                                                                                                                       064869;
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                                                                                                              01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
CITRATE (SI)-SYNTHASE (EC. 4.1.3.7) (CONDENSING ENZYME)
(CITRATE CONDENSING ENZYME) (CITROGENASE) (OXALOACETATE TRANSACETASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EEGIRFRGFSIPECQKLLPAASAGAEPLPEGLLWLLLTGKVPSKEQVDALSADLRKRASI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 DEGIRFRGLSIYECOKVLPAAKPGGEPLPEGLLWLLLTGKVPSKEOVDSLSOELRSRATV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PDHVYKTIDALPITAHPMTQFCTGVMALQTRSEFQKAYEKGIHKSKFWEPTYEDCLSLIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 NVSAHTGHLVGSPLSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVDECGENISTEQL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 NVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEVLLWIKSVVEECGENISKEQL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 KDYVWKTLNSGKVVPGFGLGVLRKTDPRYTCQREFALKHLPDDPFFQLVSKLYEVVPPIL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                    BETA VULGARIS (SUGAR BEET).
URAPUTA, VIRDIPLAMYAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEDPHYTA;
EUPHYLLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CARYOPHYLLIDAE; CARYOPHYLLALES; CHENOPODIACEAE; BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 SSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER
PLANT CELL PHYSIOL. 0:0-0(0).
--- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2800; DB 10; Length 4:
Pred. No. 0.00e+00;
34; Mismatches 27; Indels
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE CIJ-SYNTHASE (EC 4.1.3.7) (CONDENSING ENZYME)
(CITRATE CONDENSING ENZYME) (CITROGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AA; 48881 MW; 003688CE CRC32;
              437 AA
                                                                                CREATED)
           PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X84228; E137433; -. PFAM; PF00285; citrate_synt; 1. MENDEL; 15201; BETvu;2977;mn15201.
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Matches 373; Conservative
Q96544 PRELIMINARY: Q96544; Q1-FEB-1997 (TREMBLREL: C) 1-FEB-1997 (TREMBLREL: C) -FEB-1997 (TREMBLRE: C) -FEB-1997 (TREMB
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              PRELIMINARY;
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                                                                                                                                                                                                                                                         (FRAGMENT)
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SEQUENCE
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024259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
           POPULUS DELTOIDES X POPULUS BALSAMIFERA SUBSP. TRICHOCARPA.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                       121 PEMQELMRLYVTNHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEV 180
                                                                                                                                                                                                                                                                                                                                                                                      255 SDMHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALNGLAGPLHGLANQEV 314
                                                                                                                                                                                                                                                                                                                                                                                                                          181 LLWIKSVVEECGENITTEQLKDYVWKTLNSGKVVPGFGHGVLRKTVPRYTCQREFALKHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                         135 VPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEK 194
                                                                                                                                                                                                                                                                                                                     61 GIHKSKYWEPTYEDSLSLIARVPIVASYIYRRIYKDGKVIPMNDSLVIGGNFSHMLGFDS 120
                                                                                                                                                                                                                                                                                                                                            195 GIHKSKLWEPTYEDSMSLIAQVPLVAAYVYRRMYKNGNTIPKDDSLDYGANFAHMLGFSS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 PDDPLFQLVSKLYEVVPPVLTQLGKVKNPWPNVDAHSGVLLNYYGLTEARYYTVLFGVSR 300
                                                                                                                                                                                                                                                                1 MPIKEQVGALSKELRDRALVHDYVFKAIDALPVIAHPMIQFAIGVMALQVQSEFQKAYEK 60
                                                                                        LA COGNATA U., LANDSCHUETZE V., WILLMITZER L., MUELLER-ROEBER R.;
PLANT CELL PHYSIOL. 0:0-0(0).
-!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Cloning and sequence analysis of human citrate synthase cDNA.";
                                                                                                                                                                                                          61.9%; Score 2.31; DB 10; Length 339; 84.5%; Pred. No. 0.00e+00; artive 29; Mismatches 22; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.0%; Score 1997; DB 4; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51706 MW; C0532604 CRC32;
                                                                                                                                                                                  339 AA; 37834 MW; B2DA24A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 SIGICSQLIWDRALGLPLERPKSVTMELLENHCKKA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 ALGICSQLIWDRALGLPLERPKSVTMEWLENHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: TO OTHER CITRATE SYNTHASES MELL; APOY1042, G23288815. -
PROSITE; PSO0480; CITRATE_SYNTHASE; 1.
LYASE; TRICAPBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPT;
                                                                                                                                             EMBL; X84227; E276838; -. PFAM; PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITRATE SYNTHASE (EC 4.1.3.7).
                                                 /IOLALES; SALICACEAE; POPULUS
                                                                                                                                                                                                                        larity 84.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                         Local Similarity
es 284; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 AA;
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOLDENTHAL M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-HEART
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                             Query Match
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075390;
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KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERANAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY A.M., MCKENBY K., ADAMS M.D., LOFFUUS B.,
PETERSON S., PEICH C.I., MCNEIL L.K., BADGEP J.H., GLOBEK A., ZHOU L.,
OVERBEER R., GOGAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W., D'ANDREA F.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 PDEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLFWLLVTGCIPTEEQVSWLSKEWAKRAA 146
                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                       147 LPSHVVTMLDNFPTNLHPMSQLSAAVTALNSESNFAQAYARGISKTKYWELIYEDSVDLI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AQVPLVAAYVYRRMYKNGNTI-PKDDSLDYGANFAHMLGFSSSDMHELMKLYVTIHSDHE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 KLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPNDPMFKLVAQLYKIVPN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 QLKDYAWKTLKSGKVVPGFGHGVLRKTDPPYTCQPEFALKHLPEDFLFGLVAKLYEVFLG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 VLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYTTVLFGVSRALGVLAQLIWSRALGFPL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                     27 SASSINLKDILADLIPKEQARIKTFRQQHGKTVVGQITVDMMYGGMRGMKGLVYETSVLD 86
                                 Gaps
                                                                                                                                                                                                                                       AKLPCVAAKIYRNLYWEGSGIGAIDSNLDWSHNFINMLGYIDHQFTELMRLYLTIHSDHE
                                                                                                                                            34 TSSGLDLRSELQELIPEQQDRLKKLKSEHGKVQLGNITVDMVLGGMRGMTGLLWETSLLD
                                                                                                                                                                                                                                                                                                                                                                             154 VPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEFQKAYEKGIHKSKLWEPTYEDSMSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARCHAEOGLOBUS FULGIDUS.
ARCHAEA; EUFYARCHAEOTA: ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; NATURE 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
Best Local Similarity 62.2%; Pred. No. 0.00e+00;
Matches 267; Conservative 76; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42270 MW; DB9662BC CRC32;
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MEDLINE; 98049343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00285; citrate_synt; 1. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05,
08,
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Best Local Similarity 29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001011; G2649234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL.
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CITRATE SYNTHASE (CITZ)
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Pred. No. 2.12e-26;
59; Mismatches 90; Indels 18; Gaps 15;
76; Conservative 64; Mismatches 95; Indels 23; Gaps 18;
                                                                                         154 AANFLYMLHGEEPTKTAERALDMDLILHAEHEL-NASTFAARIAASTLADIYACVVAATG 212
                                                                                                                                                         243 GANFAHML-GFSSSDMHE-LMKLYVIIHSDHEGGNVSAHTGHLVASALSDPYLSFAAALN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 EEVLYLLWHGALPTGEELDAFSDELAAHRDLDDGVLDVARELAEQDESPMAALRTLVSAM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 EGLLWLLIGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAH-PMTQFATGVMAL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 SAYDESA-DFE-DV-TDR--EVNLEKAKRITAKMPSVLA-AYAR-FRRGDDYVEPDESLN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 HAANFLYMLNGEEPNEVLAETFDMALVLHADH-GLNASTFSAMVTSSTLSDLYSAVTSAI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 GTLSGSLHGGANANVMRMLKDV-DD-SDMDPTEWVKD-A---LDRGERVAGFVHRVYNVK 271
                                                 124 EGLLWLLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTOFATGVMALO 183
                                                                           97 TATSYLGSLDKKIA-VRTREETFNKAKDLIAKFPTIVAY-YHRI-RTGRNIIPPALEFSH 153
                                                                                                                                                                                   213 TLMGPLHGGAAQEVM---R-MLREVASP-RRAE--EYVKRKIEAGERIMGFGHRVYRGVM 265
                                                                                                                                                                                                           301 GLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKT- 359
                                                                                                                                                                                                                                                                                                                                                                                    CITRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).
ARCHAEA; EURYARCHAEOTA; HALOBACTERIALES; HALOBACTERIACEAE; HALOFERAX.
                       44 BEVAYLLLYGELPKKYELQDFKIELAERRELPPQI---1-GL-LT-H-LPPYTHPMVVLR 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 QVQSEFQKAYEKGIHKSKLWEPTYEDSMSLLAQVPLVAAAYVYRRMYKNGNT-IPKDDSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 YGANFAHML-GFSSSD-MHELMKLYVTIHSDHEGGNVSAHTGHLVASALSDFYLSFAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WFD II;
MADDOCKS D.G., CONNARIS H., HOUCH D.W., DANSON M.J.;
MADDOCKS D.G., CONNARIS H., HOUCH D.W., DANSON M.J.;
EMBLY AJ002075; E1154178; -.
PFAM; PF00285; citrate_synt; 1.
                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                       266 DPRAELLR-YLAKRLAAE 282
                                                                                                                                                                                                                                                                 360 DPRYTCQREFALKHLPED 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.7%;
Best Local Similarity 31.3%;
Matches 76; Conservative
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034002;
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Pred. No. 1.14e-25;
88; Mismatches 131; Indels 25; Gaps 22;
                                                                                                                                                                                                                                                                                           GERIKE U., DANSON M.J., RUSSELL N.J., HOUGH D.W.;
"Sequencing and expression of the gene encoding a cold-active citrate
"Synthase from an Antarctic Dacterium, strain DS2-3R.";
EUR. J. BIOCHEM. 248:49-57(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 VQSEFQKAYEKGIHKSKLWEPTYEDSMSLIAQVPLVAAAYVRRMYKNGNTI-PKDDSLDY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 NGDSRVPTMKS-ALDAMIKHYDRPEMLG-LYNGLEAAMEE-AKQIK-PNLDYPAGPTYNL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 KTDPRYTCQREFALKHLPED-PLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNY 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 LLIYGELPSSEQYNNFTKKVAVHSLVNERLHYLFQTFCSSSHPMAIMLAAVGSL---SAF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 EQVAYLLWNSELPNDSELKAFVNFERSHRKLDENVKGAIDLLSTACHPMDVARTAVSVLG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 EGLLWLLITGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 --AN-H-A--RA-QDSSP-EANLEKAMSLLATFPSVVAYDQRRR-RGEELIEPRED-LDY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 SANFLWM-TFGEEAAPEVVEAFNVSMILYAEH-SFNASTFTARVITSTLADLHSAVTGAI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 GANFAHMLGFSSDMHELMKLY-VT-I-HSDHEGGNVSAHTGHLVASALSDPYLSFAAAL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 GALKGPLHGGANEAVMHTFEEIGIRKDESLDEAATRSKAWWVDALAQKKKVMGFGHRVYK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 NGLAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWR--TLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTS: ALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.3%; Score 253; DB 2; Length 411; Best Local Similarity 27.4%; Pred. No. 2.11e-24; Matches 88; Conservative 93; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AB BACTERIUM;

RACULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
BEBL; U59712; G1390003; -.
PFAM: PF00285; citrate_synt; 1.
NON_TER
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) CITRATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 MGF-DIEMFIPLFIAARIIGWIAHIM-EQVADNALIRP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U85944; G2431774; -. PFAM; PF00285; citrate_synt; 1. SEQUENCE 379 AA; 41832 MW; 47DB0E16 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 AA; 46189 MW; 9CCB3291 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RICKETTSIACEAE; PICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
CITRATE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.6%;
Best Local Similarity 27.8%;
Matches 94; Conservative
                                                                                            ANTARCTIC BACTERIUM DS2-3R. BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
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                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             MEDLINE; 97454284
                                                                                                                                                                                                                                 STRAIN-DS2-3R;
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NON_TER
SEQUENCE
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Q53115
Q53115;
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Query Match 7.3%; Score 251; DB 2; Length 411;
Best Local Similarity 27.2%; Pred. No. 4.83e-24;
Matches 87; Conservative 93; Mismatches 112; Indels 28; Gaps 19;
                                                                              255 IASLWGPAHGGANEAVINMLKEIGSSENIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDL 312
                                                          145 ---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNALDFTENF 196
                                                                                                                                   197 LHMM-FATPCEKYKVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACVSTG 254
                                                                                                                                                                                                                                                  299 LNGLAGPLHGLANQEVLLWIKSV--VEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVL 355
                                                                                                                                                                                                                                                                                        313 RAAVLKETCKEVLKELGQLDGNPLLQIAIELEAIALK-DEYFIERKLYPNVDFYSGIIYK 371
                                                                                                                                                                                                                                                                                                                               357 RKTDPRYTCOREF-ALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 LLIYGELPSGEQYNNFTKQVAHHSLVNERLHYLFQTFGSSSHPMAIMLAAVGSL---SAF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 LLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSEF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 ---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNSLDFTENF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 LHMMFATPCTKYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTGI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 AHML-GFSSSD--MHELMK--LY-VTI-HSDHEGGNVSAHTGHLVASALSDPYLSFAAAL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 ASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDPR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 NGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAGULT D., FYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.; SUBMITTED (UN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLLSM.
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RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4 1 3 7) (FRAGMENT).
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411 AA; 46162 MW; 9921533A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: U59731; G1390011; --
PROSITE: PSOMB40; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt: 1.
LYASE; TRICARBOXYLLC ACID CYCLE.
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                                                                                                                                                                                                                                                                                                                                                                     372 AMGIP-SQMFTVLFAIARTVG 391
                                                                                                                                                                                                                                                                                                                                                                                                         416 YYGLTEARYYTVLFGVSRALG 436
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SEQUENCE
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Q59777
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/ Match 7.3%; Score 250; DB 2; Length 411; Local Similarity 27.2%; Pred. No. 7.32e-24; es 87; Conservative 93; Mismatches 112; Indels 28; Gaps 19;
314 AAVLKETCKEVLKELGQLDNNPLLQIAIELEAIALK-DEYFIERKLYPNVDFYSGIIYKA 372
                                                                          358 KTDPRYTCQREF-ALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNY 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 LHMMFATPCTKYKVNPIIKNALNKIFILHADHEQ-NASTSTVRIASSSGANPFACISTGI 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 KIDPRYTCQREF-ALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNY 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 NGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYAWKTLKSGKVVPGFGHGVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=M 5\6;
ROUX V, RYDKINA E., EREMEEVA M., RAOULT D.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRAIE SYNHARSE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 411 411 411 411 411 AA; 46266 MW; A54EAICF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                              411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; U74756; G1658283; --
PROSTIE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; citrate_synt; 1.
LYASE; TRICARBOXYLIC ACID CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA.
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01-JAN-1998 (TREMBLREL. 05, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                              417 YGLTEARYYTVLFGVSRALG 436
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                                                                                                                                                        373 MGIP-SQMFTVLFAIARTVG
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P77936
P77936;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 LLIYGELPATDQLAEFTHRIQRHTMLHEDLKRFYDGFPRNAHPMPVLSSVVNALSA-Y-Y 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 M-LGFSS-S-DMH-ELMK-LYVT-I-HSDHEGGNVSAHTGHLVASALSDPYLSFAAALNG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 RARIVKEQADKILVKLGGDDDLLNIAKGLEEAALT-DDYFIERKLYPNVDFYTGLIYRAL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 MTFGLPAEPYEPDPEVVRALDMLFILHADHEQ-NCSTSTVRLVGSSRANLFTSISGGINA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 LWGPLHGGANQAVLEMLEGI-RESGDDVG-GFVQK-V-KNCQAGVKLMGFGHRVYKNYDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 RYTCOREFA---LKHLP-EDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNYY 417
                                                                                                                                                                                                                                                                                          Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                         BACTERIA: FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 LAGPLHGLANQEVLLWIKSVVEECGENISKEQLKDYAWKTLKSGKVVPGFGHGVLRKTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91; Mismatches 110; Indels 26;
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BACTERIA; PROTEOBACIERIA; ALPHA SUBDIVISION; RICKETTSIALES;
                                                                                                                                                                                                                                                                          EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.;
                                                                                                                                                                                                                                                                                                       of Mycobacterium leprae.";
MOL. MICROBIOL, 7:197-206(1993).
-:- CATALYTIC ACTIVITY: CITRAIE + COA - ACETYL-COA + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 431;
                                                                                                                                     BADCOCK K., CHURCHER C.M.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                SEQUENCE FROM N.A.
PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLTRATE SYNTHASE (EC 4.1.3.7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.19e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00480; CITRATE_SYNTHASE; 1.
PFAM; PF00285; Citrate_Synt. 1.
PFASE; TRCARBOXYLIC ACID CYCLE.
SEQUENCE 431 AA, 48111 MW; ICFA87BB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 AA.
                                                                                                                                                                                                                                                                                                                                                                                               OXIDATIVE METABOLISM.
-!- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL; 299494; E350411; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.3%; Score 252;
                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: TRICARBOXYLIC ACID CYCLE
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Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                           MYCOBACTERIUM LEPRAE.
                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             93188700
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Query Match 7.2%; Score 247; DB 2; Length 411;
Best Local Similarity 26.9%; Pred. No. 2.54e-23;
Matches 86; Conservative 94; Mismatches 112; Indels 28; Gaps 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 LLLTGKVPSKEQVDSLSQELRSRATVPDHVYKTIDALPVTAHPMTQFATGVMALQVQSFF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 ---YP-DLLNFK--EADYELTAIRMIAKIPTIAAMSYK--YSIGQPFIYPDNALDFTENF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 QKAYEKGIHKSKLWEPTYE-DSMSLIAQVPLVAAYVYRRMYKNGNT-IPKDDSLDYGANF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 LHMMFATPCTKYTVNPIIKNALNKIFILHADHEQ-NASTSTVRIAGSSGANPFACISTGI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 ASLWGPAHGGANEAVINMLKEIGSSEYIPKYIAKAKDKNDPFRLMGFGHRV--YKNYDPR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 NGLAGPLHGLANQEVLLWIKSV-VEEC-GENISKEQLKDYAWKTLKSGKVVPGFGHGVLR 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 KIDPRYTCOREF-ALKHLPEDPLFQLVAKLYEVFLQFLQNLAKLNPWPNVDAHSGVLLNY 416
                                                                                                      STRAIN-NTT-118;
RAOULT D., RYDKINA E., ROUX V., EREMEEVA M., BALAYEVA N.;
SUBMITTED (JUN.1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF
                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411
46095 MW; 274AAD7C CRC32;
                                                                                                                                                                                                                                                                                                                                               -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-1- SIMILARITY: TO OTHER CITRATE SYNTHASES.
EMBL: U59726; G1390019; -.
RICKETTSIACEAE; RICKETTSIEAE; RICKETTSIA
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: U59726; G1390019; -.
PROSITE: PSOO480; CITRARE_SYNTHASE; 1.
PFAM: PF00285; citrate_synt; 1.
LYASE: TRICARBOXYLIC ACID CYCLE.
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                                                                                                                                                                                                                                                   OXIDATIVE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 4
411 AA;
                                                                    SEQUENCE FROM N.A.
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PROSITE; PS00480; CITRATE_SYNTHASE; 1.
                                      PFAM; PF00285; citrate_synt; I
HSSP; P23007; 5CSC.
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Local Similarity 68.9%;
                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                 MULTIGENE FAMILY.
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ACT_SITE
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CISY_PIG
P00889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-:- SUBUNIT: HOMODIMER.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL MAIRIX.
-:- CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                        60 SDLGKAQLGNITIDVVIGGMRGMTGLLWETSLLDPDEGIRFRGLSIPECQKLLPAAKPDG 119
                                                                                                                                                                              61 SDM-KGSIGNITVDMVLGGMRGMIGLLWKPHYLDPDEGIRFRGLSIPECQKVLPAAKPGG 119
                                                                                                                                                                                                                    120 EPLPEGLLWLLIGKVPSKEQVDGLSKELRDRATVPDYV-YKAIDALPVSAHPMIQFASG 278
                                                                                                                                                                                                                                                                                                   179 VMALQVQSEFQEAYEKGIHKSKSWEPTSEDSLNLIARVPVVAAYVYQRIYKDGKIIPKDD 238
                                                                                                                                                                                                                                                                                                                                         180 VMALQVQSEFQKAYEKGIHKSKYWEPTYEDSMNLIAQVPLVAAYVYRRMYKNGDTIPKDE 239
                                                                                                                                                                                                                                                                                                                                                                                  239 SLDYGGNFSHMLGFDDPKMLEL-MRLYVTIHSDHEGGNVSAHTGHLVASALSDPYLSFLA 297
                                                                                                                                                                                                                                                                                                                                                                                                       ALNGLAGPLHGLANQEVLLWIKSVVDECGENVITEQLKDYVWKTLNSGKVVPGFGHGVLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 KTVPRYTCQREFAMKHLPEDPLFQLVSKLYEVFLLFLQNLAKLK-PWPNVDAHSGVLLNY 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIDPRYICQREFALKHLPDDPLFQLVSKLYEVVPPILIKLGKVKNPWPNVDAHSGVLINH 417
                                                           1 MASLRSATALSRLRSRAGQGSNLSNSVRWLQMQSSADLDLHSQL-KEMIPEQQERLKKVK 59
                                                                                   5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNGER E.A., HAND J.M., CASHWORE A.R., VASCONCELOS A.C.; "Isolation of a CDNA encoding mitochondrial citrate synthase from Arabidopsis thallana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 FGLAEARYYTVLFGVSRSLGICSOLIWDRALGLPLERPKSVTLDWIEKNCKKA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLANT MÖL. BIOL. 13:411-418(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CITRATE SINTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
    78.4%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                       371; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91370823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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EMBL; X17528; E1188578; -. .. PIR; JA0149; YKMUM.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 KSEHGKVQLGNITVDMVIGGMRGMTGLLWETSLLDPEEVFALGDCRLPECQKALLPTAQS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GGLNHYRRSFVASLNWKGTL-AKSKLKH-CRKTWNRAAVSDYV-YNAIDALPSTAHPMTQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 GG-EPLPEGLL-WILLTGKVPSKEQVNSIVSGIAESGIISLIIMYTTIDALPVTAHPMTQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 PSDKSLDYGANFSHMLGFDDERLKEL-MRLTSPSTVMHEGGNVSAHTGHLVGSALSDPYL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFAAALNGLAGPLHGLANQEVLLWIKSVVEECGEDISKEQLKEYVWKTLNSGKVIPGYGH 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 GVLRNTDPRYVCQREFALKHHPDDPLFQ-CCKLMKL-ASCLTELESEEPWPNVDAHSGVL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVFFRSVSAFTRLRSRVQGQQSSLSNSVRWIQMQSSTDLDLKSQL-QELIPEHKDRLKKL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVFYRSVSLLSKLRSRA-VQQSNVSNSVRWLQVQTSSGLDLRSELVQELIPEQQDRLKKI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 82231993.
BLOXHAM D.P., PARMELEE D.C., KUMAR S., WALSH K.A., TITANI K.; "Complete amino acid sequence of porcine heart citrate synthase."; BIOCHEMISTRY 21:2028-2036(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVANS C.T., OWENS D.D., SUMEGI B., KISPAL G., SRERE F.A.; "Isolation, nucleotide sequence, and expression of a CDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 LNHYGLTEARYYTVLFGVSRSLGICSQLIWDRELLLALERPKSVTMDWLEAHCKKA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYASE; TRICARBOXYLIC ACID CYCLE; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 01, CREATED)
01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; Mismatches 76;
                                                                                                                               CITRATE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i, 954AFA81 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                        Score 2305; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS
                                                                                                    MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOCHEMISTRY 27:4680-4686(1988)
                                                                                                                                                                                                                                                                                                 472 AA; 52941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID DATA ACCOOR SOLUTION OF THE ```

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983 TAGCCGGACCACTTCATGGTTTAGCCAATCAGGAAGTTTTGGTATGGATAAAATCTGTTG 1042
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  386 AIGCICIACTATTACGCCTCAICCAAIGACTCAGITITIGCACTGGIGITAIGGCCTIAC 445
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  683 AACCAACATATGAGGATTCCATGAATCTGATTGCTCAAGTTCCACTTGTTGCTGCTGTTATG 742
  566 ITTATCGGAGGATGTATAAGAATGGACAAGTAATACCGCTGGATGACTCCCTTGATTATG 625
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  209 CTATACCTGAATGCCAGAAACTTTTACCCGGTGCAAGTGCTGGTGCAGGGCCATTGCCTG 268
   269 AAGGICTITCTITGCTICTITIAACCGGAAAGGITCCIAGCAAAGAGCAAGIAGAIGCIC 328
   443 AAGGICITCICIGCITCITITAACAGGAAAGGIGCCAICAAAAGAGCAAGIGAAITCAA 502
   329 TATCAGCAG-ATTTACGAAAACGTGCTTC-TATCCCAGACCATG-TGTACAAAACAATTG 385
  563 ATGCCTTACCAGTCACAGCTCATCCAATGACCCAGTTTGCTACTGGAGTCATGGCTCTTC 622
  206 TACAAGAATTGATTCCTGAACAACAGGATGGCCTGAAAAGATCAAGTCAGA-TATGAAA 264
   Gaps
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   Score 664; DB 27; Length 1551;
Pred. No. 0.00e+00;
0; Mismatches 261; Indels 12;
TVLFGVSPSLGICSOLIWDPALGIPLEPPKSVTMEWLEKFCKPPA"
268 c 370 g 458 t
  370 ₽
   Match 35.1%;
Local Similarity 78.5%;
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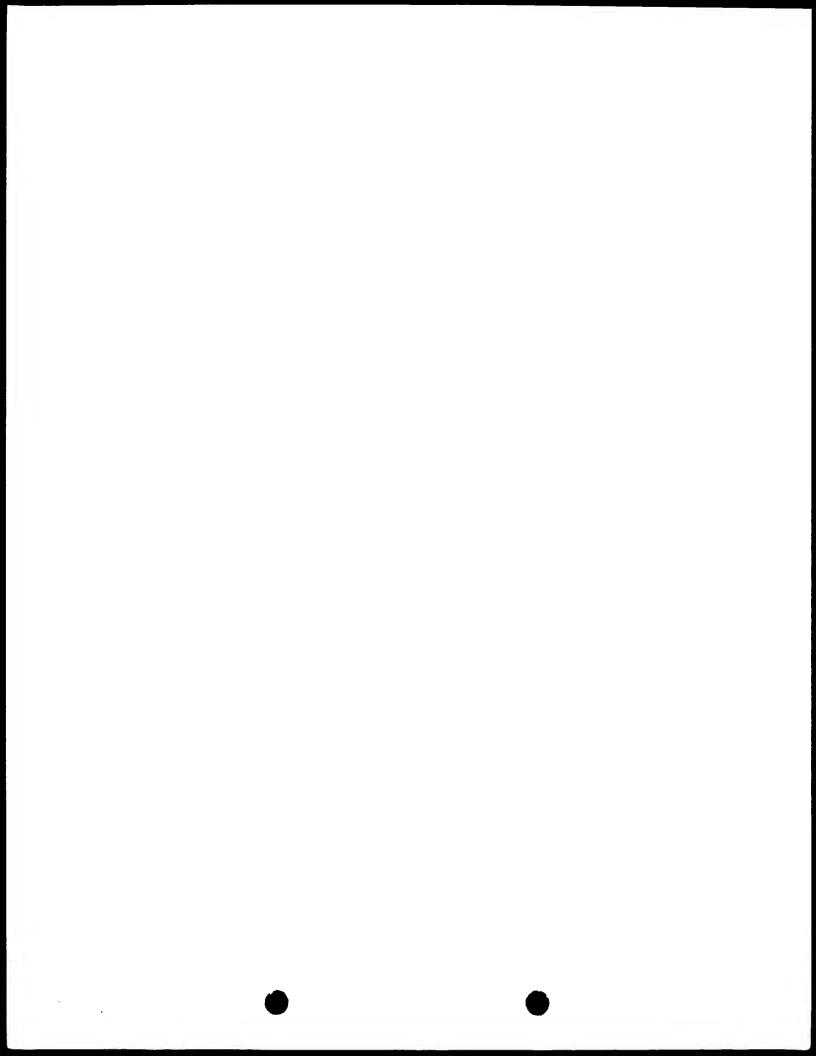
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LQELI PEHKDRLKKLK SEHGKVQLGNI TVDMV IGGMRGMTGLLWET SLLDPEEVFALG
DCRLPECQKALLPTAQSGGLNHYRRSFVASLNWKGTLAKSKLKHCRKTWNRAAVSDYV
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   Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
   Ouery Match 29.9%; Score 566; DB 27; Length 1680;
Best Local Similarity 75.6%; Pred. No. 0.00e+00;
Matches 1087; Conservative 0; Mismatches 317; Indels 34; Gaps 29;
   1 (bases 1 to 1680)
Unger, E.A., Hand, J.M., Cashmore, A.R. and Vasconcelos, A.C.
Isolation of a cDNA encoding mitochondrial citrate synthase fro
Arabidopsis thaliam Plant Mol. 13 (4), 411-418 (1989)
   1163 GATATACATGCCAGAGAGAGTTCGCTATGAAGCATTTGCCTGAAGATCCACTGTTTCAAC 1222
   1043 TGGTGTCAAAGTTGTATGAAGTGGTGCCTCCTATTCTATTAGAGCTTGGAAAGGTAAAGA 1102
   1103 ATCCATGGCCTAATGTTGATGCTCATAGTGGAGTTTTGCTGAACCACTATGGTTTGACAG 1162
   1163 AAGCAAGATACTATACGGTTTTGTTTGGGGTATCAAGGAGTCTTGGAATATGCTCACAGC 1222
  ATMICITRN 1680 bp mRNA PLN 26-NOV-1997 Arabidopsis thaliana mRNA for mitochondrial citrate synthetase. X17528
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   408 g
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  X17528.1 GI:11243
citrate synthase.
   345 c
   .1680
  1283 GGCTTGAAAA 1292
  1460 GGCTTGAGAA 1469
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  ACCESSION
  REFERENCE
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1062
   1123 GGTGTTCTGCGCAATACTGATCCCAAGATATGTATGCCAAAGAGAATTTGCCTTGAAGCAT 1182
  1063 TIGAAAGAATAIGITIGGAAAACAITAAACAGIGGCAAGGITAITICCGGGAIAIGGICAC 1122
   386
  646
  904
  166
   825
  897
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  421 CCTGGGGGTGAGC-CCTTGCCTGAAGGTCTTCTCTGGGTTCTTTTAACAGGAAAGGTGCC 479
   659 GGATICACAAATCAAAGTATIGGGAACCAACATATGAGGATICCAIGAATCIGATIGCIC 718
   177 CCTGAAGTCGCAGCTG---CAAGAGTTAATTCTGGAACACAAGGACCGTCTGAAGAAACT 233
   234 GAAGTCAGAACAIGGGAAGGICCAACIGGGAAACAICACIGIIGAIAIGGIIAIIIGGIGG 293
  294 AATGAGAGGGATGACTGGGTTGGGGAAACCTCATTGC-15GACGGGAAGAGGTA-351
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   472 ITAGCAAAGAGCAAGIIGAAGCACI-GIGGAAAGACIIGGA-AC-CGEGCIGG-TGIGGC 527
  72 AATGGTGTTCTACCGTAGCGTTTCGTTGCTGTCAAAGCTGGGGTGTGGAG--C-GGTGCA 128
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  539 TGATCATGTATACAACTATTGATGCCTTAGCAGTCAGAGGTCATGACCCAGT
  647 GAATICATAAGTCAAAGTICIGGAGCCAACATAIGAGGAITGCCTCAACCIGAITGCIC
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Cit1 gene; citrate synthase.
Cit1 gene; citrate synthase.
Populus balsamifera subsp. trichocarpa X Populus deltoides.
Populus balsamifera subsp. trichocarpa X Populus deltoides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosidae; Violales; Salicaceae; Populus.
1 (bases 1 to 1378)
La Cognata, U., Landschuetze, V., Willmitzer, L. and Mueller-Roeber, B.
2 (bases 1 to 1378)
La Cognata, U. 1378)
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  1297 CTGAACCACTATGGTCTAACCGAAGCAAGGTACTACACCGTGCTCTTTGGTGTTTCAAGG 1356
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  1417 CCAAAGAGIGITACCAIGGACIGGCIIGAAGCCCAIIGIAAGAAAGCIICAICIGCII 1474
  28-OCT-1996
  ×
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Populus deltoides"
   1238 TCACTGAGCTTGAAAGTGA-AGAACCCTGGCCAAATGTTGATGCTCACAGTGGGGTCTTG
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  Submitted (23-JAN-1995) U. La Cognata, Institute fuer
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   16. .1035
/gene="cit1"
   252 c
  Direct Submission
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   KAPAN"
   Berlin, FRG
   ĸ
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LOCUS
DEFINITION
ACCESSION
   10
   BASE COUNT
ORIGIN
  ORGANISM
   gene
  KEYWORDS
SOURCE
  AUTHORS
   REFERENCE
   AUTHORS
   JOURNAL
  REFERENCE
  JOURNAL
  CDS
   FEATURES
  VERSION
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